AF326768 Oryza sat
AP0201859 Oryza sat
16494 Sequence 14
AC026135 Homo sap1
AC02925 Homo sap1
AC02925 Homo sap1
AC02925 Homo sap1
AC05845 Homo sap1
AC05845 Homo sap1
AC05845 Homo sap1
AC025845 Homo sap1
AC025846 Homo sap1
AC02786 Homo sap1
AC07926 Trypanoso
AC07926 Trypanoso
AC07927 Dictyostell
AC010318 Rattus no
AC007928 Homo sap1
AC010188 Drosophil
AC010588 Drosophil
AC010588 Homo sap1
AL111116 Botrytis
AC011871 Homo sap1
AC014376 Homo sap1
AC014376 Homo sap1
AC014376 Homo sap1
AC014376 Homo sap1
AC013871 Mus muscu
AC005139 Plasmodiu
X63195 N. tabacum m
AC023803 Mus muscu

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Listing first 45 summaries
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Oryza sativa
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Enyza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 3896)
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Oryza sativa embryonic flower
AF326768 AF326768.1 GI:15430698
2 (bases 1 to 3896)
Moon, Y.-H., Chen, L.
Direct Submission
                                                                                                                                                        Aubert,D., Chen,L., Moon,Y.H., Martin,D.,
and Sung,Z.R.
                                                         1487698
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AL591122
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AC0106185
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AC0116518
AC010618518
AC01061855
AB010068
                  Sung, Z.R.
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protein mRNA,
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AL596170 Listeria
AY023518 Oryza sat
AF429315 Homo sapi
AC053543 Homo sapi
AC053543 Homo sapi
AC090668 Homo sapi
AC103789 Homo sapi
AC103789 Homo sapi
AC103789 Homo sapi
AC355547 Human DNA
AC016272 Homo sapi
AC016272 Homo sapi
AC09855 Rattus no
AB0103459 Plasmodiu
AF269518 Staphyloc

PLN 05-SEP-2001 complete cds.

Yang, C.H.

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FEATURES
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Best Local Sim
Matches 3894;
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FRWDCSKCLDKLKTSDNGTAPRTLPAKQNGTSDGCSIFTYBSTGYPASVGSQKVSPS
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RENAADPCEDDRSTIFYPMEVSMDIPVSMLTYBGGKCEQICNEPCEVVLKRSSKK
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OHYSELSTRCGLTSCSDLNRIGSKTTADDDCVIVAAKDGSDYASSVFDTNSQQKSLAS
QSTQKELGGHLALTTQESPHPQNFQSTGPQQTHLRMEEWYITAASSPLESHHDDQYIA
EAPTEHWGRKDAKKLTWEOFKATTRNSBAATGGAQFRGGTQAVDLTSTHWMSSSNYA
SRQPYLAPLDRYABATARGAGATSTSYGSNLNGKIFUTF
EDLSRHQLHDLPLRFAPHPRYGVLGSLTAMESBNCGTQSGYKLGVSTGTSHQM
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1920	tatggtggtgaaagcaccagaaatggtcagaacatacatgtactcagcgcagaagatcaa	1861	Db Qy
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1860	tcaaaggggaaaacagcgggtttgagtaaggggaaaacacattcagctgctagtaccaaa	1801	P 9
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1800	aatatgcataagacagatgtctgtcagcatgtatcagaaatctccacacagaggtgctca	1741	ру
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1740	acacccactgcgagtactcagcatgatgatgagaatgatactcaaaatggtcttgacaca	1681	Db Qq
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(E-mail:tsasaki@abr.affrc.go.jp,

URL:http://www.dna.affrc.go.jp,
URL:http://www.dn
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Varnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa genomic DNA, chromosome 1, PAC:clone:P0485D09
AP001859
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This sequence of this clone has an overlap with P0431F01 clone, This sequence of the 3' end. This clone ends at the position 57,376 DDBJ.AP001550 at the 3' end. This clone ends at the position 57,376 of P0431F01. Detailed information on overlap and assembly quality together with annotation of this entry at together with annotation of the entry at together with annotation of this entry at together with annotation of the entry at together with annotation of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ehrhartoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 150594)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sativa (cultivar: Nipponbare) DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(7919. .7964,8092. .8280,8453. .8473,8558. .8610)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HRRVLAVLIPEVDIRRRVLAYVGFYVVASMSIVLGCFRIGHVRSPNPGQIRLQQIKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ∕organism="Oryza sativa"
STSAAFVSRFGNF"
join(10735. .1)
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                                                                                                                                                                                                                                                                                                                             codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:7630233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150594 bp
           .10850,10933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                .10987,11596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone: P0485D09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome 1, PAC
                .11653,12285. .12379
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CDS

CDS

CDS

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CDLQVNANFDKNEAHDSQSSMG-PQACYTSAEAVASALFAVHCHYSSSNLDPDOHLQED
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KLHFMSEADFNSPNCLKSELNQDI SLOGLLSGPDAVEADS I SKSNHQSDVY SSEADTH
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AEVYTQSSSSGDAEMFANPGCSNDERHVPSSTMESI FPCGDQOYTNAEEPFEASLEKEP
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NVCTPMRLMGSPTHDESTGVLLKSAAKSFICTPSILKKRHTDLLSPI FDKRI EKKYGT
EKDRGVSDTSSTGIQTSCI INATKDDALITTVLR I ERSASSKSLEKKLVFSDENKENLG
EKDRGVSDTSSTGIQTSCI INATKDDALITTVLR I ERSASSKSLEKKLVFSDENKENLG
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SIGMNGOIANNATPPAQCTVNYGIAIYLYIYISQFFSYTIIPIIGCQNHACPCLCSV*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          region of the predicted gene.
Similar to Caenorhabditis elegans chromosome 3, cosmid C17C10; alcohol dehydrogenase/ribitol dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YTTEQTKDGQSAGNDEHMDEQTTGERSSATNVATNDDLSGNLVSTSSF"
complement(join(18608..18823,19905..20031,20072..2022
20774..21113,21407..21738,21975..25508))
/note="ESTs AU082761(S5084),D42006(S5084) correspond to
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PLNEYSANCNSSPAMTQQNSEDSGCFAVREVENSSGCSQSSLAKVSCSQVHDTTVPLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPWSKEEDEIIVQMVNKLGPKKWSTIAQALPGRIGKQCRERWYNHLNPGINKEAWTQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRRSTKGNWTPEEDAILSRAVQTYNGKNWKKIAECFPDRTDVQCLHRWQKVLNPELVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAA94769.1"
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join(23045. 23145,24592. 24670,25118. 25216,25302. 2541
25608. 25750,26364. 26445,27073. 27158,27527. 27760,
29332. 29917)
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DYQGGSNVLKHLGYYSMIGLLRIHCLLGDYRTGLKCLAPIDLNQQGVYTIVIGSHISA
IYHYGFANLMMRRYAEAIREFNKILLYILKYKQYHKKSPQYDQILKKNEQMYAFLAVC
IYHYGFANLMMRRYAEAIREFNKILLYILKYKQYHGKSPQYDQILKKNEQMXAFLAVC
ISLCPQHNLIDENVSTQLKEKYNDKMYKMQRTDEETYAAYDELFSYACPKFITPSPPA
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PTYYAGMNDLSQKMYGLSMQDSSYMGMNSSPYSTTPSSSSSMGQPSKPEDKLFGDLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T19C21; unknown protein.
/codon_start=1
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/db_xref="GI:7630238"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (028739)"
                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30166. .30675
/note="ESTs AU031545(E61825), AU031546(E61825) correspond
                                                                             complement(join(34629. .34795,36831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="Similar to Arabidopsis thaliana chromosome 2 BAC 19C21; unknown protein. (AC004683)"
/note="hypothetical protein"
                                                                                                                             IAKTKQNKA"
                                                                                                                                                                                                                                                                                                                                                                               /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene.
                                                                                                   .36867,38803. .38895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4, BAC
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CDS

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Query Match 75.8%;
Best Local Similarity 87.4%;
Matches 3487; Conservative
54044 ATGCATCTTTATAATGATAATCTTATTTTTCTTGTACCAGAGGGTATGTTGCTCTTCTTC 54103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                      386 acgaaccggcacaacaccaatgcgagcatttctccataagagggtatgtttgctcttcttc 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DQEGARVVGTNCMLARGGTGAVAPVLELTATPRODAAAEAGVDEPAGHQCEHESIRGY
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TWHIEVNGADQPPSTPKLSEVVLKRNEDENGKTEETLVAEQCNLTKDPNPMSGKERDQ
VAEQCNLTKDPKPVSGGKCEQILOEPCEEVVLKRSSKSKRKTDKKLMKKQOHSKKRTA
QADVSDAKLCERKPKKVRLLSEIINANQVEDSRSDEVHRENAADPCEDDRSTIFVPME
VSMDIPVSNHTVGEDGLKSSKNKTKRKSDVDDGSSLMWLNGKKKRTGSVHHTVAH
PAGNISNKKVTPTASTQHDDENDTENGLDTNHKTDVCQHVSEISTQRCSSKGKTAGL
SKGKTHSAASTKYGGLESTRRGVTMIDDIPMDIVETENSVLSHAKVSPAEHDIQIN
SDLHEOSLFYKKKKOKLEVTREKQTMIDDIPMDIVELLAKNQHERGLMTETDCSDINR
IQSKTTADDDCVIVAAKDGSDYASSVFDTNSQQKSLASQSTQKELQGHLALTTQESPH
PONFOSTQEDQOTHLRMEEMVTIAASSPLFSHHDDQYIASASTTADDFRONDERDTENGCHASSTARGNAKCKTRGVHTDDIPMDIVETENGCHALTTQESPH
PONFOSTQEDQOTHLRMEEMVTIAASSPLFSHHDDQYIASASTARGHERGKAKKTTRGSPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(58634..58667,58796..58902,59018..5908
59368..59432,59385..59648,60333..60442,60620..60707,
60835..60945))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KATTRNSPAATCGAQFRPGIQAVDLTSTHVMG$SSNYASRQPVIAPLDRYAERAVNQV
HARNFPSTIATMEASKLCDRRNAGQVVLYPKESMPATHLLRMMDPSTLASFPNYGTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGCFMEKDLIFMTHGRGVVKADEEVRGSRSARTELKIRGVGLMLVDCGYPPIHVGVDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(46367. .46423,47537. .47769,48031. .48153,50082. .5
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54084. .54514,54601. .55709,56020. .57468)
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MTVVRCTTRQRLLEGERIQCDIRGKKILGSKGPFDSQNRKNTGI
EIEVGLLDACVIVYTVEKPENERRIKKHGRLRGLSRLCDRLGPKLVWDPSPTKVVTPY
VQFPRCHTLPHRG"
                                                                                                                                                                                                                                                                                                                                                        join(69755. .69967,70096. .70236,70344. .70514)
note="Similar to Arabidopsis thaliana chromosome 1 BAC
F19P19; unknown protein (AC000104)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNFSANVSVDGSVVNLGLWDTAGQEDYSRLRPLSYRGADVFILSFSLISRASYENVQK
KWMPELRRFAPGVPVVLVGTKLDLREDRAYLADHPASSIITTEQGEELRKLIGAVAYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"ESTs AU082698(R0665),D23963(R0665) correspond to a region of the predicted gene. Similar to Arabidopsis thallana rac GTP binding protein Arac7. (AF079484)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEYMDYR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNQMESQLHNSQYAHNQYKGSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPLRPHPR
VGVLGSLLQKEIANWSENCGTQSGYKLGVSTG;TSHQMNRKEHPEALNSGMFSAKWNA
LQLGSVSSSADFLSARNSIAQSWTRGKGKMVHPLDRFVRQDICITNKNPADFTTISND
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1 (bases 1 to 7218)
Dorner,F., Scheiflinger,F. and Falkner,F.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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                                                                                       Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhgh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Garad-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Klein, J., Larocque, K., Lamazares, R., Landers, T., Lehoczky, J., Klein, J., Leu, C., Lilu, G., Locke, K., Macdonald, P., Marguis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Maldrin, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oilvar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Tijilio, J., Yo, W., Thimission
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Submitted (19-MAR-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 5, 2000 this sequence version replaced g1:7264205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Primates; Catarrhini; Homi
1 (bases 1 to 141041)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 3, clone RP11-78022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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Eutheria; Primates; Catarrhini; Hominidae;
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RP11-78022
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center project name: L7353
Center clone name: 78_0_22
Chemistry: bye-terminator Big Dye; 100% of reads
Consensus quality: 132847 bases at least Q40
Consensus quality: 137397 bases at least Q30
Consensus quality: 137397 bases at least Q20
Consensus quality: 137097 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Insert size: 13941; sum-of-contigs
Quality coverage: 4.8 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
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54230 64518: contig of 10289 bp in length
64519 64618: gap of 100 bp
64619 79904: contig of 15286 bp in length
79905 80004: gap of 100 bp
80005 109945: contig of 29841 bp in length
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19509 26115: contig of 6607 bp in length

26116 26215: gap of 100 bp

26216 39655: contig of 13440 bp in length

39656 39755: gap of 100 bp

39756 54129: contig of 14374 bp in length
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2191 2290: gap of 100 bp
2291 5642: contig of 3352 bp in length
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14920. .19408
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Homo sapiens chromosome 3q clone RP11-78022, WORKING
SEQUENCE, 10 unordered pieces.
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Albrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,Z., David,R., David,R., David,R., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo: 1 (bases 1 to 141095)
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FOSTER, P., Frantz, P., Gabis, A., Gao, J., Garcia, A., Garner, F., Garreal, J.H., Guevara, W., Ginaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Judah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Lewis, L. Li, J., Li, X., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucler, A., Lucler, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, N., Morgan, M., Mouris, S., Moser, M., Nickerson, E., Nokabbat, K., Moyyen, N., Niew, G., Miner, G., Miner, Z., Mitchell, T., Nohabbat, K., Moyyen, N., Niew, S., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quil, M., Okwuon, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Rulz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, R., Wang, S., Ward, Moore, S., Warren, R., Washington, C., Walliams, G., Williamson, A., Walezyk, R., Wooden, S., Wolley, K., Ward, M., W., F., Zhou, J., Zorrilla, S., Nelson, D., Ninson, R., Walliams, G., Williamson, A., Wleczyk, R., Wooden, S., Wollston, D., Welson, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
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                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 141095)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: Phrap; version 0.990329
Consensus quality: 138822 bases at least Q40
Consensus quality: 137507 bases at least Q30
Consensus quality: 138991 bases at least Q30
Consensus quality: 138991 bases at least Q30
Estimated insert size: 139059; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 4.8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center clone name: RP11-78022
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34465
69011
69111
84564
84664
99241
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69010:
69110:
84563:
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                                                                contig of 34364 bp in 1 gap of unknown length bicontig of 34546 bp in 1 gap of unknown length contig of 15453 bp in 1 gap of unknown length contig of 14577 bp in 1 contig of 14577 bp in 1
                                gap of contig
of
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JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

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REFERENCE
AUTHORS
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SOURCE
ORGANISM
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AL591122/c
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                                                                                             COMMENT
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                                                                                                                                                   JOURNAL
                                                                                                                                                                       TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11650 CTGATGGAGAAAATCTGTAAAGCTGATTAAATATTCATTTAATAGTTG!TTCCTGAAGATA 11591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11770 AAAAAAGTAAATTGGCATTAGGAAAAACATTGTAAAGGAAGAGGGTAAATAGTTAACAA 11711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1478 taagcatggatattcctgttagcaaccatacagtgggagaagatgggttaaaatcaagta 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1418 gtgaaaatgccgctgatccctgtgaggatgatagaagtaccatcccggtcccgatggaag 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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Local Similarity 46.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atactgaaaatggtcttgacacaaatatgcata 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACATTGAAGCAACAAAACAGAAAAAATTATTTAAAATTACAAATTATCAAAATATTCTGG 11531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggctgaatggaaaaagaaactggaagtgtgcatcacacagtttgctcatccagctg 1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggaatttgagcaacaaaaagtgacacccactgcgagtactcagcatgatgatgagaatg 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATAGAAAATCAAAACCAAACCAGTTAGACTTAAAAAAAGATATTAAAAAAGATTTGAAAAAC 11651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agaacaagacaaaacgcaaatactctgatgttgtagatgatggatcatcacttatgaact 1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAACAAAATTGATTCTATTGAAAATTCATA 11498
                                                                                                                                                                                                                                                                                                                                      189409 bp DNA linear HTG 18-JAN-
Homo sapiens chromosome 1 clone RP11-415K20, *** SEQUENCING IN
PROGRESS ***, 3 unordered pieces.
                                                     Center: Wellcome Trust Sanger Institute
                                                                                       Submitted (17-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: Clonerequest@sanger.ac.uk On Nov 12, 2001 this sequence version replaced g1:16304972.
Contact: humquery@sanger.ac.uk
                                     Center code:
                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                        HTG;
                                                                                                                                                                                                                                                                                                                        AL591122.13 GI:16904444
                   Web site:
                                                                                                                                                                       Direct Submission
                                                                                                                                                                                        Martin, S
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123171
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129354
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134226
134326
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                                                                                                                                                                                                                                                                                                      HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="3q"
                 http://www.sanger.ac.uk
                                                                           ---- Genome Center
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134225: contig of 4772 b
134225: gap of unknown 1
134325: gap of unknown 1
138699: contig of 4374 b
138799: gap of unknown 1
141095: contig of 2296 b
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contig of 13447 bp in
gap of unknown length
contig of 6083 bp in
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FEATURES
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ORIGIN
                                                                                                                                                                                                         Db 137087 CAGGGGTGGATGGAGCTGGTGCACCAGGGGTGGACAGAGGAGACGCACTAGGGGCGGATG 137028
                                                                                                                                                                                                                                                                                  Db 137147 ATAGCGATGCAGCGAAGCTGGATGGAGCTGGTGTACCAGGGGTGGACGGAACGGATGCAC 137088
                                                    RESULT 7
AC055845/c
                DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XCAP4; version 4.5
Sequencing vector: M13; M77815; 0% of reads
Sequencing vector: plasmid; L08752; 99% of reads
Sequencing vector: plasmid; L08752; 99% of reads
Sequencing vector: plasmid; 0% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 187859 bases at least Q40
Consensus quality: 188342 bases at least Q40
Consensus quality: 188672 bases at least Q20
Insert size: 189209; sum-of-contigs
Insert size: 199247; 1.3% error; agarose-fp
Quality coverage: 10.90x in Q20 bases; sum-of-contigs Quality
coverage: 10.95x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                   gtggtggaactggtgctgtagcgccagtgttggagctgacagcgacgcctcgtcaggatg 364
                                                                                                                                    GAGCTGATGCACCAGGGGTGGACGGAGC 137000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: bA415K20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                      Homo
                                      AC055845
IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47654 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128066 128165: gap of
128166 187247: conti
187248 187347: gap of
187348 189409: conti
                                                                                                                                                                                                                                                                                                                                                               1.2%;
ilarity 57.4%;
Conservative
                  sapiens chromosome 11 clone RP11-682B13 map 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment:04137
fragment_chain:1"
187348. .189409
/note="assembly_fragment:04057"
46587 c 48574 g 46393 t
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/clone_lib="RPCI-11.2"
1. .128065
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128166. .187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment_chain:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment:03248
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      œ
    unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of 2062 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   left"
                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                      Score 47.2; DB Pred. No. 0.32;
                                            151076 bp
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bp in length
                                                                                                                                                                                                                                                                                                                                                                        63;
                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 others
                                                                                                                                                                                                                                                                                                                                                                                                            Length 189409;
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                              HTG 21-JAN-2002
, *** SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                            Gaps
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SOURCE
ORGANISM
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AUTHORS
TITLE
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VERSION
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Dodge, S., Domino, M., Doyle, M., Ferredra, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Klein, J., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McDan, P., McGurk, A., McKernan, K., Pierre, N., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pierre, N., Pierre, N., Pierre, N., Pierre, N., Pierre, N., Schauer, S., Severy, P., Spencer, B., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
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Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choepel, Y., Colangelo, M.,
Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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Center clone name: 682_B_13
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Location/Qualifiers
                                                                                                                                                26513: gap of 100 bp
142582: contig of 16069 bp in length
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                                                 AL Submitted (21-MAR-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

On Dec 6, 2001 this sequence version replaced gi:13429999.

On Dec 6, 2001 this sequence version replaced gi:13429999.

Genes were predicted from the integrated "Esults of the following: GENSCANI.0, BLASTN2.0, BLASTN2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/Dlast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without almost the entire length of partial sequence) is classified as an 'unknown' protein a gene wedicted with a gene predicted as an 'unknown' protein a gene predicted with a gene protein an order of the protein as consensed to the protein and the protein but with EST homology (covering almost the entire in A gene without a gene predicted as an 'unknown' protein a gene predicted with a gene predicted as an 'unknown' protein a gene predicted with a gene protein to the protein and the protein as the protein as the protein and the protein as classified as an 'unknown' protein a gene predicted as an 'unknown' protein as a gene predicted with a gene protein and 'unknown' protein but with a gene protein as classified as an 'unknown' protein but with a gene protein and 'unkn
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Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 145120)
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is classified as a 'hypothetical' protein
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/chromosome="11"
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                               protein. A gene predicted with a gene prediction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Embryophyta; Tracheophyta; a; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone: P0452F10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAC
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824 others
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Clone:P0452F10.
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MEFGKRIRQVFGRVTGWSVSKTEDIFVVTVRKXLRTVTTGSNSI
NIVVVVDGKSAVRMPFVRAMRALVLAAACTECLARTR"

join(10963 . 11280,12207 . 12285;12396 . 12531,13093 . 13288,
13475 . 13543,13695 . 13834,14005 . 14127,14970 . 15162,
16452 . 16614,17013 . 17056,17279 . 17369,18595 . 18738,
18827 . 118866,23823 . 23963,24033 . 24075)
/gene="P0452F10.4" . 23963,24030 . 24075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAPILVVYSSAVACASARLLLGRHARPCTAAPVYLSVAGSLVMILNPLDQYYYYY*
complement(join(9838. .9932,10020. .10126,10340. .10380,
10459. .10464))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(3049.
5211. .5279
                                                                                                LCTREAMNVMQHQQKGGHVFNMDGAGSGGSSTPLTAVYGSTKCGLRQFQASLLKESRR
SKVGVHTASPGMVLTDLLLSGSSLRNKQMFNLICELPETVARTLVPRMRVVKGSGKAI
NYLTPPRILLALVTAMVRRGRWFDEEGRAVYAAEADRIRNWAESRARFSFTDAMEMYT
                                                                                                                                                                                         GEEASSSPPPPTTAEARRRKGPLYKLKAAIQGLAGSRSAAAEAYGGEYQRAVEKAEE
IFFSVATQVGRYVITMMSSGVVLGVGFQLSGGDSQMNTLIWYSMLGGVILGTMICAKS
VLEEHCKAGFRANVITGSPESYLQTINELEENIQEGLSVAKKKOREILLHAKVYGTSC
DVCKPEDVKKLVNFAKDELGSIDIWINNAGTNKGFRPLVNFSDEDISQIVSTNLVGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           jóin(10963. .11280,12207. .12285,12396. .12531,13093. .1
13475. .13543,13995. .13834,14005. .14127,14970. .15162.
16452. .16614,17013. .17056,17279. .17369,18595. .18738.
18827. .18866,23823. .23963,24030. .24075)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="P0452F10.1"
join(8115. .8396,9324. .9341)
/gene="P0452F10.2"
                                 ENTWVSVFSLSVVCAFIILSSSVARLHRMLQPPIELKPCRVMILLDGEAGRSLHLVQT
MYGFLCASHFFNIAIIMYIHATARPVQIIPMWRGVHPEQWLMCLEVNDFFGFLTRLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similar to Arabidopsis thaliana hypothetical protein F17N18.140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="1"
WSHGGIHVVMYFISHDKCRREKGHSSRSNPPFTDAWDPPRSNATLTQVTVARNAPAII
                                                                                                                                                                                                                                                                                                                       /protein_id="BAB78667.1"
/db_xref="GI:17385727"
/translation="MAAAAVVHLSVHGRLRRSPELHARPYHRPSLLRCRAFKQEADNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(8115. .8396,9
/gene="p0452F10.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Rice myb-related
includes stop codon(s)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="contains EST AU064167(E4058)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="P0452F10.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="BAB78666.1"
/db_xref="GI:17385726"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="P0452F10.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAB78665.1"
/db_xref="GI:17385725"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="P0452F10.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(3049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation-"MPRRTPAAAAVHTTRRLSRLPLESPSSTWERAEAAAADRAGVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lement(join(9838. .9932,10020. .10126,10340. .10380,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . .3420,4142. .4504,4612. .4878,5066. .5206,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .3420,4142. .4504,4612. .4878,5066. .5206,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .8396,9324. .9341)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SITEPAARS PASTAGAS AGALARY
SITEPAARS PASTAGAS AGALARY
SITEPAARS PASTAGAS AGALARY
SITEPAARS PASTAGAS AGALARY
KRAHHHHHEPPPEPEPHLLHYYGHPPPEPEPEFKOHYGGVYGWOONG PEPEPDHY
LKKVESHES PASTE PASTAGAS AGALARY
LKKVESHES PASTAGAS AGALARY
ATDGFSDANLLGOGGFGYVHKGYLPNGTEVAVKQLRDOSGQGEREFQAEVEIISRVHH
KHLYFLYGYCISGGKRLLVYEXVPNNTLELHLHGRGRFTMEWFFTLRIALGAARGLAY
LHEDCHPKIIHRDIKSANILLDARFEAKVADFGLAKLISDNNTHYSTRYMGTFGYLAP
EYASGGQLTEKSDYFSGYMLLEIITGRRFVRSNOSOMDSILVDWARFLMMRASDDGN
YDALYDPRLGQEYNGNEMARMIACAAACVRHSARRFRMSQVVRALEGDYSLDDLNEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDARQIPETEMEMGSLKKDGDSNGTRDSQAS"
join(30710..30762,30889..30915,31041..31140,32690.
32922..33008,33095..33234,33611..33710)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative receptor protein kinase PERK1"
/protein_id="BAB78668.1"
/db_xref="GI:17385728"
/translation="MSSPSSPPPANQTATPPPANQTAAPPPASNNSSSPPAPGSLSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(24964...25375,26027...26542,27087...27173,27278...2
27728...27804,27960...28107,28553...28714,28954...29274)
/gene="P0452F10.5"
/codon_start=1
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27728. .27804,27960. .28107,28553. .28714,28954. .29274)
/gene="P0452E10.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="p0452F10.6"
join(30710. .30762,30889. .30915,31041. .31140,32690. .32836,
32922. .33008,33095. .33234,33611. .33710)
/gene="p0452F10.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRPGHSRFLGSYNSNEYDTGHYNEDLKKFRKMAFGSGNLESSQQTQPTEFVPNRSVSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAMRARDAAFASRARVRMAERLIYGRDMVFAPYGEFWRQARRVSVLHLLSPRRIASFR
GYREQEVAALLDRVRRRCGVRGGGETVNLSDLLMSYANGVISRAAFGDGAYGLDGDEG
GEKLBELFANFEALLGTATVGEFVPWLAWVDKLMGLDAKAARISAELDGLLERVIADH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protéin_id="BAB78670.1"
/db_xref="G1:17385730"
/translation="MEISSSLAAVLHSPLFILLAALLILLPVFTLLSFSSAKKPGDGGGW
/translation="MEISSSLAAVLHSPLFILLAALLILLPVFTLLSFSSAKKPGDGGGW
RLPLPPSPRGVPFLGHLPLLGSLPHRKLRSMAEAHGPVMLLWFGRVPTVVASSAASAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGFNVEAAFECIARNAIKNEPEEEIIFLIQLMLEVLEGNSARQAVNARRYGTSDIAS"
join(34853. .35557,36458. .37129)
/gene="P0452F10.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MASRRRWLLKVIILGDSGYGKTSLMNQYVNKKFSNQYKATIGAD
FLTKEVQIDDRLFTLQIWDTAGQERFQSLGVAFYRGADCCVLVYDVNVTKSFERLNSW
REEFLIQASPSDPENFPFVVLGNKIDVDGGNSRTVSEKKAKAMCASKGNIPYFETSAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="RAS-related GTP-binding protein Rab7 family"
/protein_id="BAB78669.1"
/db_xref="GI:17385729"
                                                                                                                                                                                                                                                                                                                                                                      LYHFDWELPHADGAAAATAARLDMGELFGLSMRMKTTLNLVAKPWSSDV"

join(39698. .40690,40829. .40832,42030. .42769)

/gene="P0452F10.8"

join(39698. .40690,40829. .40832,42030. .42769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RERRRLSQPDGGDGDGDENVDHRDFVDVLLDVSEVEBGAGAGEVLLFDTVA1KAII
RERRRLSQPDGGDGDGDENVDHRDFVDVMKLJQCEIRAAVGVPGASGGAEVTEDHLGE
LDMLTAAATDTTFTTLEWAMELINH PVMKKLJQCEIRAAVGVPGASGGAEVTEDHLGE
LRLLRAVVKETLRLHAPVPLLVPRETVEDTELLGYXVPARTRVIINVWAIGROAAWG
DRAEEFVPERWLDGGGEEVEYAAQLGQDFRFVPFGAGRRGCPGAGFAAPSIELALTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative cytochrome P-450LXXIA1 (cyp71A1)
family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Join(34853. .35857,36458. .37129)
/gene="P0452F10.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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                                                                            EVMRTRDLAFASRPRVRMSERLFYGRDMAFAPYGEFWRQARRVTVLHLLSPRRVLSFR
GVREQEVAALLDRVRRRCGGGGETVNLSDLLMSYAHGVISRAAFGHGGAHGFDGDEGG
VPRVTCMNERFIEQDMMAAGTDSSFTTTEWVMAELINHPRVMRKLQDEIRAVVGTSSA
                      EKLRÄLFADFEGLLGTMTVGEFVPWLAWVDKLTGLDAKVARTSAAMDGLLERVIADHR
ERRRSRGQAVGDGEADADHRDFVDVMLDVSEAEEGAGAGAGGVLFDTVAIKAVILSKK
                                                                                                                                /translation="melsslaallhsplllavlllvfswllvsstkkrppppcgDggr
Rlplppsppgvpllghlpllgtlphrklrswaeahgpvwllrlgrvpavyassaaaae
                                                                                                                                                                                                                                                                                                                                            /gene="P0452F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="contains EST C98812(E3123)"
                                                                                                                                                                                                                                                                                                                      /note="contains EST C98812(E3123)"
                                                                                                                                                                                      /db_xref="GI:17385731"
                                                                                                                                                                                                               /protein_id="BAB78671.1"
                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                     putative cytochrome P-450LXXIA1 (cyp71A1)
                                                                                                                                                                                                                                                                                                                                                        .40690,40829. .40832,42030.
2F10.8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
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VERSION
KEYWORDS
SOURCE
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AX083744/c
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                                                                                                                                        464 totgotototatotoggattttocatgaccagaaaaaatgtgatgaacacaaagotagtt 523
                                                                                                                                                                                                                                              404 aatgcgagcatttctccataagagggtatgttgctcttcttcagaagaaggatccaaaat 463
                                       524
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        WWTNHAKRGATMCWYWYWTGTNRRWCMRTYAMRTWYTRSNANWSCATKBMWWTMKWYATK 1032
                                                                                           YRTAWYAMWCAWRNNNMWCATNGYAKSCATNNAMWYATTRWAAYAAAKWARWAGNNMRMY 972
                                                                                                                                                                                                                                                                                                                109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoters"
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1.2%;

Score 45.2; DB Pred. No. 0.63;

6;

Length 1141; Indels

344;

Mismatches

560;

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Gaps

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32 c

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832 others

and

B.n. FAE1

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Db 134344 TGCCGGCCCATTTTCACTTCCAAACTTTCGACCGTGAGATTCCTCCTCATGCTTGGAAAT 134403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               522 ttcaagcccattttctgtagcaaagtttcgacgatgggattgctcgaagtgcttggataa 581
                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTGAAAAATTCAGATCAT 134422
                                                                                                                                                                                                                                                                                                                                                                                                                                                           gttgaaaacttcagataat 600
                                                                                                                                                                                                                                                                                         1141 bp
sequence 22 from Patent W00111061.
AX083744
                                                                                   Regulation of embryonic transcription patent: WO 0111061-A 22 15-FEB-2001; UNIVERSITY OF BRITISH COLUMBIA (CA)
                                                                                                                                                                                                                synthetic construct
                                                                                                                                                   Kunst, L. and Clemens, S.
                                                                                                                                                                    artificial sequence.
1 (bases 1 to 1141)
                                                                                                                                                                                                                                  synthetic construct.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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RTRVIINVWAIGRDAAAWGDSAEEFVPERWLDGGGGGVEYAQQLGKDSRFVPFGAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(48011. .48970,51142. .51771)
/gene="P0452F10.9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative cytochrome P-450LXXIA1 (cyp71A1) family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="contains EST AU163704(E4276)"
/organism="synthetic construct"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAB78672.1"
/db_xref="GI:17385732"
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                                                1. 1141
                                                             Location/Qualifiers
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2F10.9"
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Pred. No. 0.98;
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                            YWYWRYDYWCAMCWMNAKAKVRTAMKHMWYYTDRYVSANNTGVRWMMMRWCMW
                                                                                                                                                                                                                                                                                                                                                                                                                        cagaaattataaatgctaaccaggttgaggattctagaagtgacgaagttcat 1416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtgagcagatctgcaatgagccatgtgaagaagttgttctcaaagaagctccaaatcta 1243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gtgatggttgctccatcacatttgttcggagcacttttgtgcctgctagtgtttggttccc 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNYKYCYAYBWYYBMYMGKHHWBWWRRABHRSWNMWWVKCRNKYMVSWHYHAMRYBKWAB 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agaggaagacggataagaagttgatgaagaagcagcagcacagcaagaaacgcactgccc 1303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atcaggttgctgagcagtgcaatttgaccaaagatccgaaaccagtgtctgggcagaaat 1183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVGCNNNWKDRMAHHHWCATNNNMMWWWYAYMHHMHKKGKAAWTNNKTABRDDHBAHVKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMWAAGASNBVTYNWCWRMTYMGKTMTNNNNNNKAWYYRTKTVAWCNNRYYYDTAVWTBK 252
  1 (bases Martin,S.
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 93100)
                                                                                                                                                                                                                                   Human DNA sequence
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1 clone RP1-220G17
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chromosome llpl2-14.1,
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66244 CCATTCTTGCAGGAGTAAGGTGGTCTCATTGTGGTTCTAATTTGCATTTCCCTGATAA 66303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Aug 20, 2001 this sequence version replaced gi:15029116.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SMISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aacttctagcaggaaccagatggagtctcaacttcataattctcagtatgcacataatca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gtacaaaggatcaaccagcacatcatatggcagtaacctgaatggaaagattccattgac 2978
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                                                                                                                                                                                                                                                                                                                         AATTGTCTATTTAT
                                                                                       ACO87825 114980 bp Homo sapiens chromosome 11 clone sequence, 3 unordered pieces.
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AC087825.2 GI:14192972
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RP1-220G17 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP1-76K20 is at 91101 in this seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP1-220G17 from the library RPCI-1 constructed by the group of Pieter de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMPORTANT: This sequence is not the entire insert of clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   true right end of clone RP1-296L11 is at 2000 in this sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP1-220G17"
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15637 c 16764 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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52.1%;
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Pred. No. 1;
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                                                                                                                            RP1-220G17
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TITLE
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Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,
McPwan,P., McEwan,P., McKernan,K.,
McPwan,P., McEwan,P., McKernan,K.,
McPwan,P., McEwan,P., McEwan,P., McEwan,P., McMenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pterre,N., Pollara,V., Raymond,C., Retta,R.,
Phunkhang,P., Pterre,N., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
Roy,A., Santos,R., Schauer,S., Schupback,R., Seeman,S., Severy,P.,
Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Milson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zembek, L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (28-JAN-2001) whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA on May 24, 2001 this sequence version replaced gi:12584323. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S. Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Girbhan, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRoque, K., Lamazares, R., Landers, T., Johnson, R., Landers, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 114980)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP1-220G17
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                           be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 114348 bases at least Q40
Consensus quality: 114583 bases at least Q30
Consensus quality: 114709 bases at least Q20
Insert size: 115000; agarose-fp
Insert size: 114780; sum-of-contigs
Quality coverage: 10.3 in Q20 bases; agarose-fp
Quality coverage: 10.3 in Q20 bases; sum-of-contigs
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------ Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WIBR
                                                                                                                                                            1 5011: contig of 5011 bp in length
5012 5111: gap of 100 bp
5112 73744: contig of 68633 bp in length
73745 73844: gap of 100 bp
73845 114980: contig of 41136 bp in length
                                                                                                        Location/Qualifiers
∕organism="Homo sapiens"
                                                               .114980
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                                                                                                                                                                                                                                                                                                         DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McSwan, P., McGurk, A., McKernan, K., McChan, C., Marquis, N., McSwan, P., McGurk, A., McKernan, K., McChan, C., Marlor, T., McGurk, A., McKernan, K., McChan, C., Marlor, T., McGurk, A., McKernan, F., McGurk, A., Marlor, T., McGurk, A., McKernan, F., McGurk, A., Marlor, T., McGurk, A., McKernan, F., McGurk, A., McKernan, F., McGurk, A., Marlor, T., Marlor, T., Marlor, T., McGurk, A., Marlor, T., Marlor, T.
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theoc Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Cooke, P., Choepel, P., C
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homó sapiens, clone RP11-15F4
                                                                                                                                                               McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
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/chromosome="11"
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WORKING DRAFT SEQUENCE, 2 ordered
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  CCATTCTTGCAGGAGTAAGGTGGTGTCTCATTGTGGTTCTAATTTGCATTTCCCTGATAA
                                                                                                                      aacttctagcaggaaccagatggagtctcaacttcataattctcagtatgcacataatca
                                                                                                                                                                                                                             tgcgacgcatcttctgagaatgatggatccatcaacattagcaagcttccccaactatgg 2858
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                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 163000; agarose-fp
Insert size: 158292; sum-of-contigs
Quality coverage: 13.8 in Q20 bases; agarose-fp
Quality coverage: 14.2 in Q20 b.
NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                               48372 a
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39274: contig of 39274 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: M13; M77815; 36% of reads Sequencing vector: Plasmid; n/a; 64% of reads Sequencing vector: Plasmid; n/a; 64% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 158197 bases at least Q40 Consensus quality: 158232 bases at least Q30 Consensus quality: 158245 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: 13455
Center clone name: 15_F_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39275 39374: gap of 39375 158392: cont
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             vector_side:right"
1 27087 c 29475 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-15F4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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Pred. No. 1.1;
                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                          Length 158392;
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  89184
                                                                                           89124
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MEDLINE
REFERENCE
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
SH1UL45A/c
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BASE COUNT
ORIGIN
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ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
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                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                    gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (01-DEC-1993) Hansi J. Dean, Virology Swine Research Unit, U.S. Department of Agriculture, Ames, IA 50010, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHIUL45A 3400 bp DNA linear VRL 28 Pseudorabies virus helicase (UL5) and UL4 genes, complete L20708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virology 202 (2), 962-967 (1994)
94303212
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Dean,H.J. and Cheung,A.K.
Identification of the pseudorables virus UL4 and UL5 (helicase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudorabies virus (strain Indiana-Funkhauser) DNA
Pseudorabies virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 3400)
                                                                                                                                                                                                                                                        /gene="UL4"
2777. .3214
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/db_xref="GI:431466"
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CDALAPGRVTIQHGPVLTVLAVDGEPERCSYVEARTWPAAPEGALVMPFSTWSCAERS
RRLRGPAGGLLATLVAERALHVTITAYRPDVLRDALREARILE"
a 1241 c 1160 g 497 t
                                                                                                                                                                                                                                                                                                                                                                                                                      PRAWEKSLAAADNPVDIEALELPFAAYLISGNAGSGKSTCIQTLNETMDCVVITGSTR
VAAQNVYAKLSAAYSSRYVNIT FQEFGFRGHIVQAAQLGRYSVACPTSPPTVRELQKRD
LVYYWEVLQDISRRVLAGSHEEFARLERLTIGRAAEHLAFACHGSLPAFARSNIV
IDEAGLLGRHLLTAVVYCWWLLNAAVDTTQYAARARPVLVCYGSPTQTDSLESRFEHA
RQLCRVRASENLLTYLITNRALREYTDLSRNWAIFINNKRCQEYEFGELMKALEYGLP
LTDEHLRLUDSEVVPERYINNPANLQGWTRLYSSHREVSAYMSRLHAHLKVAGDAQFV
VFTLPAYTIVRTAAFDXYREATQAPHLTLDRWLAANGRITNYSQSRQDAAALRCEA
RAQGGVVLARCEVTYVLNSQVAVTTRLKKLVIGFSGFTEAFAAVLRDDAFVHAQGGSA
RAQGGVVLARCEVTYVLNSQVAVTTRLKKLVIGFSGFTEAFAAVLRDDAFVHAQGGSA
EYTYRFLSSLLESGMIAFYNFLQRPGLAPEAVVAAYRRLAAVVAAALRVPEEHFDFSG
AAAPAAPAGPGGAADDDDDLFAALSENMLDMLYCHYDFARPETTSEYYAQFLMKKTLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="helicase"
/protein_id="AAA50986.1"
/db_xref="GI:456681"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="UL5"
217. .2718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Pseudorabies virus"
/strain="Indiana-Funkhauser"
/db_xref="taxon:10345"
                                                                                                                                                                                                                                                                                                                                                                            THATAPAFAEELARRKLHAGTAELLASLDTPRVVLRDQSGFLSILNVNLSDFVESLDD
                                                                                                                                                                                                                                                                                                                                                                                                  ADRYAALSELFGPAFARAPFETHVDSVSVRGCEVFVGGLRGALLSTALQTDSYTLVGY
                                                                                                                                                                                                                                                                                                                               LRMNMNPLREEPERDNGISEHILAALRDGAVHIVY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MAAAAAAEGPRATNATYLNFTSMHGVEPIVERVRELAATPAEAP/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="UL5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                             codon_start=1
                                                                                                                                                                                      'note="putative"
                                                                                                                                                                                                         'function-"unknown"
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AC107868/c
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 ctcgtggtggaactggtgctgtagcgccagtgttggagctgacagcgacgcctcgtcagg 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        722 TGCAGCACCTCCCAGTAGTACACCAGGTCGCGCGCTTCTGCAGCTCGCGCACCGTCGGCGGG 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 tggagattgttgcagtagatcaggagggaggtcgtgttgttgggacgaactgtatgcttg 301
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Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C.,
Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Severy, P., Spencer, B., Stange-Thomann, N., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus clone RP23-405A17, LOW-PASS SEQUENCE SAMPLING. AC107868 AC107868 I GI:18308571
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87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., BoguslavKiy,L., Boukhqalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Brown,A., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Cocke,P., DeArellano,K., Gage,D., Galagan,J., Gardyna,S., Cord, G., Cord, E., Cord, Cord
                                                                                                                                                                                                                                                                                                                                                                                                             All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (24-JAN-2004) WILLCHIEGO LINGE, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren,B., Linton,L., Nusbaum,C. and Lander,E. Mus musculus, clone RP23-405A17
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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NOTE: This record contains 81 individual
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                                                                          Center project Information Center project name: L20687 Center clone name: 405_A_17
                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (24-JAN-2002) Whitehead Institute/MIT Center for Genome
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                                                                                                                                                                                                                                                                     http://www-seq.wi.mit.edu
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Pred. No. 1.
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sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
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However, it should not be assumed that this clone
Will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the record is updated, the accession number will
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63 22562: gap of 100 bp

53 23301: contig of 739 bp in

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33 9642: contig of 710 bp in le
33 9742: gap of 100 bp
43 10445: contig of 703 bp in le
46 10545: gap of 100 bp
46 11257: contig of 712 bp in le
47 1273: gap of 110 bp
48 1273: contig of 716 bp in le
49 1273: gap of 100 bp
70 12173: gap of 100 bp
71 12173: gap of 100 bp
71 12173: gap of 717 bp in le
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6340: contig of 720 bp
41 6440: gap of 100 hr
7172: con+4
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82 19996: contid of 715 bp
97 20096: gap of 100 bp
97 20802: contid of 706 bp
03 20902: gap of 100 bp
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8105: gap of 100 b
8832: contig of 727
8932: gap of 100 b
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4701: contig of 710 bp
801: gap of 100 bp
5520: contig of 719 bp
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13570: contig of 580 bp i
3670: gap of 100 bp
14394: contig of 724 bp i
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77119; gap of 100 bp
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           Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20
This sequence is the entire insert of clone RP5-897D18 The true left end of clone RP11-4603 is at 76409 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality sa an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gcacagcaagaaacgca 1297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human DNA sequence from clone RP5-897D18 on chromosome; part of a gene for a putative novel protein, EST, STSs complete sequence. AL133232
AL133232.15 GI:8649008
                                                                                                                                                                                                                                                                                                                        Submitted (14-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestes: clonerequest@sanger.ac.uk
On Jun 21, 2000 this sequence version replaced gi:8574104.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
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Direct Su
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              //www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                       9448. 9450
/note-"Tandem repeat. Forced join. Approximately 350 bases missing according to restriction digest data"
                                                                                                                                                                                                                                                                                                                                                                                                    8410. .8697

/note="AluJb repeat: matches 1. .

8708 .8867

/note="MLTIJ repeat: matches 48.
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/db_xref="taxon:9606"
/chromosome="20"
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ADIR repeat: matches 26. .

5332. .5406

Chote="12 repeat: matches 2617.
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8326. .8397
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/note="AluJo repeat: matches 1.
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/note="AluSp repeat: matches 1.
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                                                                                                                                                                                   /note="AluJb repeat: matches 1.
11021. .11313
                                                                                                                                                                                                                                       note="MIR repeat: matches 51. .155 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L2 repeat: matches 1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MLT1C repeat: matches 1.
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note="MER3 repeat: matches 5. .203 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="MER58A repeat: matches 60. .216 of consensus"
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                                                        note="L1MD2 repeat: matches 6052. .6326 of consensus"
                                                                                          note="Alux repeat: matches 1. .311 of consensus"
                                                                                                                              e="AluSx repeat:
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12727. .13033
note="Alusz repeat: matches 1. .308 of consensus"
                              note="match:
                                                                                                                                                                                                                                                                                    note="AluSq repeat:
25996. .26231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluSx repeat: 9072. .19149
         /evidence=not_experimental
                                                                                                                                                     'note="AluSc repeat: matches
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                            ESTs: Em:AI377332*
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..... repeat: matches 1. .224 of complement(join(<28867. .28921,29503. ./gene="dJ897D18.1" /note="L1MD2 repeat: matches 5502. .5934 of consensus" /note="AluSg repeat: matches 1.
27855. .28078 /note="Aluy repeat: matches 1. .310 of consensus" 18394. .18501 | Inote="MER45B repeat: matches 926. .1039 of consensus" /note="match: GSS: Em:AQ077906"
17944. .17994 /note="AluSx repeat: matches 3. 8047. .18078 note="16 copies 2 mer tt 84% conserved" 'note="AluSq repeat: matches 1. note="L1MC3 repeat: matches 7160. .7451 of consensus" 26370. .26427 note="LIMC3 repeat: matches 7451. .7735 of consensus" note="Alusg/x repeat: matches 92. .309 of consensus" 'note="AluSx repeat: matches 3. 'note-"AluJb repeat: matches 1. note="MER20 repeat: matches 54. 22190. .22419 0252. .20359 note="L2_repeat: matches 2130. note="MLT2B repeat: matches 1. 'note="L2 repeat: matches 2628. note="L2 repeat: matches 2635. note="MIR repeat: matches 20. 'note="AluY repeat: matches 1. note="Alusx repeat: matches 1. 168. 19949 te="L2 repeat: matches 2233. 50. .20251 e="MADE1 repeat: matches 1. e="240 copies 2 mer aa 64% conserved" 3. .14269 e="L2 repeat: matches 2323. .2750 of consensus" 9. .14778 "AluSc repeat: matches 76. .135 of consensus" .26736 Alujb repeat: matches 1. .17436 repeat: matches 1. matches 78. matches 1. matches 40. .293 of consensus" 135. .154 .310 of .311 of consensus" 262 of consensus" .312 of consensus" .237 of consensus .310 of consensus" .2233 of consensus .444 of consensus" .2702 of consensus" .2693 of .134 of consensus" .296 of consensus" .296 of consensus" .302 of consensus" .2628 of consensus" .304 of consensus" .80 of consensus" .215 of .296 of consensus" of consensus" consensus" consensus " consensus"

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Search completed: September 16, 2002, Job time: 15337 sec
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                                                                                                                                                                                                                                                                                                                                                       14699 AAAAGAAAGAAAGAA 14715
                                                                                                                                                   1756 gatgtctgtcagcatgtatcagaaatctccacacagaggtgctcatcaaagggggaaaaca 1815
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complement(join(28867. .28921,29503. .29930))
/gene="dJ897D18.1"
30614. .30718
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/note="AluJo/FRAM repeat: matches 192. .286 of consensus"
30946. .31076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 73. .179 of consensus"
30788. .30845
/note="29 copies 2 mer at 72% conserved"
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                 20:36:45
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Result
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Maximum Match 100%
Listing first 45 summaries
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/SIDS1/gcgdata/geneseq/geneseqn·emb1/NA1981.DAT:*
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2456
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ABL06814
AAC44195
AAS75925
AAS75925
AAH54196
AAC32967
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ABL34172
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Drosophila melanog
Drosophila melanog
Arabidopsis thalia
DNA encoding novel
DNA encoding novel
S. epidermidis gen
Human wild-type pr
Human cancer assoc
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	AAI18167	AAK37335	AAK11566	ABA30385	ABA63135	AAI00573	AAI31897	AAI10643	AAK26014	AAK00565	ABA22091	ABA52290	AA107733	AAI56167	AAI47330	AAI27301	AAI22038	AAK50216	AAK41287	AAK24165	AAK15554	ABA40197	ABA34204	ABA75585	ABA67114	ABA49199	AAH48024	AAA29550	AAI94740	250	AAV63196	AAZ38223	AAS92080		ABL32775	ABL34624
	Probe #8100 for ge	Human bone marrow	Human brain expres	Probe #8851 for ge	1 11v	Probe #564 used to	Probe #583 used to	Probe #576 for gen		Human brain expres	#557 fo	8		Probe #24853 used	used	for	~	Human bone marrow	3		expre	#18663 for	Probe #12670 for g	foetal	foetal	Human breast cell	Internal control B	HIV codon altered	Human neuroblastom	Human immune syste	cDNA from clone fp	Human S184L mutant	DNA encoding novel		immune syst	Human metastasis a

ALIGNMENTS

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RESULT 1
ABL06815/c
               WPI; 2001-656860/75.
P-PSDB; ABB62712.
                                                                                                                                                                                                         Drosophila melanogaster expressed polynucleotide SEQ ID NO 14927.
                                                                                                                                                                                                                                             ABL06815;
                                                                            23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                            WO200171042-A2.
                                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                           26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                               ABL06815 standard; cDNA; 1788
                                                                                                        23-MAR-2001; 2001WO-US09231.
                                                                                                                          27-SEP-2001.
                                                                                                                                                                              pharmaceutical; gene;
                                          Venter JC,
                                                           (PEKE ) PE CORP NY
                                           Adams M,
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                                           PWD,
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New isolated nucleic acid detection reagent for detecting 1000 or more

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Best Local Similarity
Matches 130; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful in developmental blology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins

[ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 14927; 21pp + Sequence Listing; English
                                                              23-MAR-2000;
11-JUL-2000;
                                                                                                     23-MAR-2001;
                                                                                                                               27-SEP-2001
                                                                                                                                                        WO200171042-A2
                                                                                                                                                                                 Drosophila melanogaster
                                                                                                                                                                                                        pharmaceutical; gene;
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                                                                                                                                                                                                                                              Drosophila melanogaster expressed polynucleotide SEQ
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          JC,
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ilarity 47.3%;
Conservative
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             Adams
                                                            2000US-191637P
2000US-0614150
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                                                                                                                                                                                                                                                                       (first entry)
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          PWD,
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Pred. No. 0.17;
0; Mismatches
          Myers
            EW;
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invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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P-PSDB; ABB62711.
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 25-FEB-1999;
05-MAR-1999;
                                                                                                                                                                        Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway;
                                                                                                                                                                                                                   Arabidopsis thaliana DNA fragment SEQ
                                                                                                                                                                                                                                                                                                     AAC44195 standard;
                                           25-FEB-2000;
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                                                                                                  EP1033405-A2
                                                                                                                                Arabidopsis
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                                                                                                                                                           pathway;
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 99US-0121825
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                                                                                                                                                            promoter;
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31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                              1251 gacggataagaagttgatgaagaagcagcagcacgcaagaaacgcactgcccaggctga 1310
                                                                   W0200175067-A2
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                             30-MAR-2001; 2001WO-US08631.
                                               11-OCT-2001
                                                                                     Homo sapiens
                                                                                                                Human; chromosome mapping;
                                                                                                                                   DNA encoding
                                                                                                                                                      13-FEB-2002
                                                                                                                                                                                           AAS90679 standard; cDNA; 246 BP
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14-OCT-1999;
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                                                                                                       supplement;
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77; Conserv
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                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                 novel human diagnostic protein #26483
                                                                                                                                                                                                                                                                                                                                                                                                        99US-0161361.
99US-0161920.
99US-0161992.
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99US-0158369.
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99US-0160989.
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                                                                                                     e mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                    1.18; 57.58;
                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                    Score 42.8; DB Pred. No. 0.095;
                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                             DB 21;
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11-OCT-2001.

WO200175067-A2

30-MAR-2001; 2001WO-US08631.

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;

SS

DNA encoding novel human diagnostic protein #11729

13-FEB-2002

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fig. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations
                                                                                                                                                                                                                                                                                                    AAS75925 standard; cDNA; 2456 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 246 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags polymucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 26483; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-639362/73.
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                                                                                                                                                                                                                                                                                                                                                                                                               69;
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CC Steel The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the company of 
RESULT 6
AAH54196/c
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Matches 69
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23-AUG-2000;
                                                                                                                                                                                                                                                                                               AAH54196 standard;
                 WO200134809-A2
                                                                                                                                                                                                              03-SEP-2001
                                                                                                                                                                                                                                                         AAH54196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2456 BP; 656 A; 575 C; 654 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention
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                                                          Staphylococcus epidermidis
                                                                                                                         Staphylococcus
                                                                                                                                                                 S. epidermidis
                                                                                                     vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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2000US-0649167.
                                                                                                  endocarditis; ds.
                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                 genomic polynucleotide sequence SEQ ID NO:3560
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s useful as hybridisation probes
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                                                                                                                         infection; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1) and (11) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (1) may be used to produce the S. epidermidis polypeptides (11) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (11) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4455 to 4472, no sequences are present for SEQ ID NO:4455 to 4472.
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Best Local Similarity
Matches 105; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH52304 to AAH53970 represent nucleic acids (I) encoding (II), given in AAG81454 to AAG83120, from Staphylococcus (I) and (II) can have antibacterial activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-316495/33
                                                                  09-FEB-2000
                                                                                                                                     AAZ32967 standard;
                                                                                                                                                                                                                                                                                             1901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctcctagcacacaatcatctcaagggaagaatgctgatagatcaactcttccaaagagtg 772
                                                                                                                                                                                                                          ATCTAATTAATAAGAACAAGACATCTGCTTA
                                                                                                                                                                                                                                                                                                                                                                                      tgcaagaaggcaatgactccaaatgcaatgcgccttctggcaagaatggagctgctgagg 832
                                                                                                                                                                                                                                                                                                                                                                                                                                   CTATAAGTGAAAAAGCAATCGAACGTAAAACAGGAGCGCGTGGATTACGTTCAATTATAG 1962
                                                                                                                                                                                                                                                       caaatgtctctgaggacaacacttctgttga
                                                                                                                                                                                                                                                                                               TCATTACTGAACAAACAATTAATGAAGAAATTGAGCCTGAATTATATGATGAAGGAA 1842
                                                                                                                                                                                                                                                                                                                                                                Page 1144-1145; 2188pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.1%;
                                                                                                                                       DNA;
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Human wild-type protein kinase MKK4 gene fragment E

MKK4; mitogen activated protein kinase; MAPK; MAPK pathway;

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CC also involved in suppressing a variety of tumours. MKK4 is a dual Cc specific kinase that activates Jun kinases (ERKS) which are a subgroup of extracellular signal-regulated kinases (ERKS) which are a subgroup of MAPKS. The JNK and p38 MAPKS are activated via dual phosphorylation CC on threonine and tyrosine and then go on to activate proteins further CC downstream in signal transduction pathways. Tumour suppressor genes such CC as MKK4 are deleted at high frequency in certain tumour types. The CC as MKK4 are deleted at high frequency in certain tumour types. The CC deletions often involve loss of a single allele, which is known as loss of heterozygosity (LOH), and the remaining allele is presumed to be non-functional, either because of a pre-existing inherited mutation, or CC decises of a secondary sporadic mutation. Alternatively, the deletion cCC may involve deletions spanning many megabases of DNA, while homozygous deletions spanning many megabases of DNA, while homozygous deletions spanning many megabases of DNA, while homozygous concessed to the MKK4 locus or its expression product in a tissue sample for the diagnosis and prognosis of human cancer, and can cc sample for the diagnose of a predisposition to breast, pancreatic, colorectal and testicular cancers, as specific MKK4 mutations have been found in cell lines derived from such tumours. MKK4 oligonucleotides are useful for the detection of the mutations to breast, pancreatic, cc colorectal and testicular cancers, as specific MKK4 mutations have been found in cell lines derived from such tumours. MKK4 oligonucleotides are useful for the detection of the mutations of the MKK4 gene or mRNA.

CC MKK4 allele via PCR, and can be used as probes to detect point mutations, PCR amplification for cancer therapy. MKK4 gene or mRNA.

CC MKK4 protein may be used for screening of drugs which can restore MKK4 gene or mRNA.

CC may find the man cancer which result the function of the MKK4 gene or mRNA.

CC may find the man cancer which result the function of the m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Columns 71-74; 63pp; English
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       trom a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein kinase, MKK4, which includes exon E. The gene comprises ag exons. MKK4 (also known as JNKK1 and SEK1) may be involved in (mitogen-activated protein kinase) pathway for the signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phorylation; Jun kinase; JNK; p38; tumour; suppressor; of heterozygosity; LOH; cancer; detection; diagnosis; prognosis; st cancer; pancrastic cancer; colorectal cancer; testicular cancer; screening; gene therapy; protein replacement therapy; mimetic; ds.
   mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYRIAD
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   in
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/note= "MKK4
368..2167
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1..247
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the MKK4 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or a portidiagnosis,
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AAA09310-20 are novel genes isolated by SEREX screening from a renal cancer cell line 1973/10.4. The genes encode cancer associated antigen precursors. These gene products are useful in methods for preventing, diagnosing and/or treating disorders, especially cancer, associated with abnormal expression of human cancer associated antigens. The method comprises contacting a sample from a subject with an agent that specifically binds to the nucleic acid molecule or expression product (or fragment) complexed with a human leukocyte antigen (HIA) molecule and determining the interaction between the agent and the nucleic acid
                                                                                                                       Claim 57; Page
                                                                                                                                               abnormal expression
                                                                                                                                                          Preventing,
                                                                                                                                                                                                                      Stockert
                                                                                                                                                                                                                                   Obata Y,
                                                                                                                                                                                                                                                                                05-OCT-1998;
05-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic;
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DB; AAY92346.
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                                                                                                                                                                                                                                 Gout
                                                                                                                                               diagnosing
pression of
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Chen
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                                                                                                                       84; 121pp; English
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98US-0166350
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/transl_except=
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Y, Old
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                                                                                                                                               and/or treating human cancer as:
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Jager E,
                                                                                                                                                                                                                                                                                                                                                                                        (pos:281..286, a
(pos:401..406, a
(pos:620..625, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor DNA, clone NY-REN-62
                                                                                                                                                                                                                                                                                                                                                                                                                          (pos:38..43, aa:Gly)
(pos:59..64, aa:Gly)
                                                                                                                                                 associated
                                                                                                                                                          disorders associated
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aa:Lys)
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Best Local
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can be including eye are including eye are.
                                                                                                                                                                                                                                                                 The present invention provides a number of human immune system as genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorticluding eye diseases such as retinopathy, neovascular glaucoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1956 ctcggcaaaggtttctccagctgagcatgatatccaaaattatgtcttgaccttcatgagca
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                                                                                      Nucleic acid comprising frag
for diagnosis and treatment
                                                                                                                                                                   30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                               Claim
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                                                                                                                                                                                                                                                                                                                                        Human
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98; Conserv
                                                                                                                                                   EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 989
                                                               SEQ ID
                                                                               methylation
                                                                                                                                  Piepenbrock
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP;
                                                                                                                                                                                             2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                       system associated gene SEQ ID NO:
                                                                                                                                                                   2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                         (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression
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                                                              2145;
                                                                                                                                                                                                                                                                                                                                                                                          DNA; 15518
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                                                                                                                                                                                                                                                                                                                                                        entry)
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                                                                                      fragment of chemically modified ment of diseases associated with
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                                                              32pp + Sequence Listing;
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; Pred. No. 0.53
0; Mismatches
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No. 0.
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             anaemia,
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.53;
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                                                              German.
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                                                                                                                                                                                                                                                                                                                        antiasthmatic;
                                                                                        gene, us
                                                                                                                                                                                                                                                                                      anaemia;
                                    The sequences
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                            disorders,
           myeloid
                                             associated
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Matches 1
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                         01ek
                                                                                                                                                                                                                                                                                                  Metastasis associated cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukaemia, Alzheimer's disease, AIDS, rheumatoid arthritis, psoriasis and in diseases. The present sequence is a go
                                                                Claim 1;
                                                                                  also
                                                                                          New nucleic acid derived from chemically treated metastasis useful for diagnosis of cancers by analysis of cytosine meti
                                                                                                                                                                                                                           06-APR-2001;
                                                                                                                                                                                                                                                               WO200177376-A2
                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                              Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgtgtgtttgtgtgtgtttttgtaggggttcgttgtagttgttttgggtgtttggtt 14884
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116; Conservative
                                                                                                                                                          EPIGENOMICS
                                                                SEQ
                                                                                  treatment
                                                                                                                                                                                                                                                                                                                                                                                     standard;
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                                                                                                                                        Piepenbrock
                                                                                                                                                                            ; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
                                                                                                                                                                                                                           2001WO-EP03970
                                                                ID NO 177;
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP;
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; Pred. No. 4.2;
0; Mismatches
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                                                                                                                                                                                                                                                                                                  cytostatic; ds.
                                                                                                                                                                                                                                                                                                                             gene
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                                                                Sequence Listing; English.
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inflammatory/ulcerative bowel
gene of the invention.
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                                                                                                                                                                                                                                                                                                            gene therapy; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  15048
                                                                                                                                                                                                                                                                                                                                                                                                                                                    234
                                                                                           methylation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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The present invention provides a number of human metastasis associated genes which are modified by cytosine methylation. The sequences can be used in the diagnosis and treatment of cancer. The present sequence is one of the genes of the invention.

Sequence

15518

BP;

3047

362

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4183

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7926

0 other

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RESULT 11
ABL32775/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective; anti-HIV; anticonvulsant; ophthalmológical; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL32775 standard; DNA;
                                                              The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinepathy, neovascular glaucoma and megalar decorations.
                                                                                                                                                                                                                               WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                        02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune system associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                            Claim 1;
                                                                                                                                                                                    Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
              diseases.
                         macular degeneration, arteriosclerosis, anaemia, cancer, acute mye leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune system disease; cytosine methylation; antiasthmatic;
seriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                        methylation
                                                                                                                                                                                                                                                          Piepenbrock C,
                                                                                                                                            SEQ ID NO 748;
              The
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             present
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             sequence is a gene of the invention.
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                                                                                                                                            32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                          Berlin
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Pred. No. 4.
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                                                                                                                                                                                       gene, us
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                                                     acute myeloid
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RESULT 1
AAH54703
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Matches 95
                      AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15122 BP; 3782 A; 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S. epidermidis
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                                                                                                                                                                                                                                               Claim 8; Page 1752-1753; 2188pp; English.
                                                                                                                                                                                                                                                                                        Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                     Kimmerly WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                 09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200134809-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH54703
                                                                                                                                                                                                                                                                                                                                                                                                                                              09-NOV-2000; 2000WO-US30782.
AAH55098 represent oligonucleotide sequences and primers in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                  (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agacaac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for vaccinating
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95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic polynucleotide sequence SEQ ID NO:4067
                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0164258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.0%;
                                                                                                                                                                                                                                                                            polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
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No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92;
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                 which
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                   are
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   RESULT 13
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                       31-MAR-2000;
23-AUG-2000;
                                                                                                   biodiversity
                                                                                                                                                                 P-PSDB;
                                                                                                                                                                                                     Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic of
                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3257
                                                                             Claim 1;
                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                               WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                               (HYSE-)
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                                                                                                                                                                              2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96; Conservative
                                                                                                                                                                  ABG27893.
                                                                                                                                                                                                                               HYSEQ
                                                                          SEQ ID No 27884; 103pp; English
                                                                                                                                                                                                                                                       2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                               INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA;
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Pred. No. 2.4;
0; Mismatches
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  sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for identifying expressed genes. (I) is useful in gene therapy techniques ct to restore normal activity of (II) or to treat disease states involving C(II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in Cd diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and classification actid sequences. AAS64197-AAS94564 represent novel human chia diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fifth the patent of the patent directly from WIPO at fifth the patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fifth the patent did not appear in the printed specification, but was obtained pet_sequences.
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Best Local S
Matches 79
                                                                                                                                                                                       exon
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                             13-JUN-1997;
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                                                             23-NOV-1999
                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                 loss of heterozygosity; LOH; cancer; detection; diagnosis; prognosis;
breast cancer; pancreatic cancer; colorectal cancer; testicular cancer;
                                                                                                                                                                                                                                                                                                                                                               somatic; signal transduction; apoptosis; stress; cytokine;
phosphorylation; Jun kinase; JNK; p38; tumour; suppressor;
                                                                                                                                                                                                                                                                                                                                                                                                                               Human S184L mutant protein kinase MKK4 gene fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ38223;
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                                                                                            US5989885-A
                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                              MKK4; mitogen
                                                                                                                                                                                                                    intron
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                                                                                                                                                                                                                                                                                                                  screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGTGTATCTTCAAGCCAAGCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAAAAAACACAGATGTTTCTACAAACCAA
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79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                activated protein kinase;
                               97US-0874186
                                                                                                                                                                                     /*tag= a
248..367
                                                                                                                                        /note= "MKK4
368..2167
                                                                                                                                                                                                                                                                                                                 gene therapy;
                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 A; 212 C; 190 G; 259 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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Pred. No. 1.2;
0; Mismatches
                                                                                                                                                         mutant
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                                                                                                                                                                                                                                                                                                                 protein replacement therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                mutation;
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10-JAN-1997;

97US-0782482

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RESULT 1
AAV63196
ID AAV6
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CC MKK4 is also involved in suppressing a variety of tumours. MKK4 is a dual codon transduction of cytokine-induced and stress-induced apoptosis.

CC MKK4 is also involved in suppressing a variety of tumours. MKK4 is a dual codon transduction of cytokine-induced apoptosis.

CC MKK4 is also involved in suppressing a variety of tumours. MKK4 is a dual codon transduction and then go on to activate proteins further codon threonine and tyrosine and thanses (ERK3) which are a subgroup codon threonine and tyrosine and thanses (ERK3) which are a subgroup codon threonine and tyrosine and thanses (ERK3) which are a subgroup codon threonine and tyrosine and thanses (ERK3) which are a subgroup codon threonine and tyrosine and thanses (ERK3) which are a subgroup codon stream involve loss of a single allele, which is known as loss of heterozygosity (LOH), and the remaining allele is presumed to be consisted of the consisting allele is presumed to be deletions of the mocaygous deletion of both alleles. LOH events commonly complete of the diagnosity sporadic mutation. Alternatively, the deletion commonly completed eletions spanning many megabases of DNA, while homozygous codeletions are relatively small in size, probably due to the proximity of essential genes. Sequences derived from the MKK4 gene can be used to consent the diagnosis and proquests of human cancer, and can useful for the diagnosis of human cancer, and can be used for screening of drugs which can restore MKK4 gene or mRNA.

CC MKK4 proteins can be used for screening of drugs which can restore MKK4 gene therapy, protein mutation of the M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Page -; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skolnick MH, Perry WL,
AAV63196 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a mutation in the MKK4 gene.
This sequence is not shown in
                                                                                               ataagttttacaaatatgtatatagtgt 318
                                                                                                                      gtaattaccataaggaggtttatagtgt 3757
                                                                                                                                                                                                                                                           tattgtatttccattttaagtaaaggcaaggtgatatttaagatgtataagaataacaga 230
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                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene fragment E shown
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      2522
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Pred. No. 2.4;
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                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      347 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the specification, in columns 71-74.
                                                                                                                                                                                                                                                                                                                                                                                                                                        769
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Best Local Similarity 47.4
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                      The present sequence encodes a secreted protein. The nucleic acid sequence is isolated from a human adult placenta cDNA library using probe AAV63206. The polypeptide may have biological activities such has e.g. nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, haemostatic activity, chemotactic/chemotkinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity or other activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agostino I
Racie LA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  haematopolesis regulating activity; tissue growth activity; activininiblin activity; chemotactic; chemokinetic activity; haemostatic; thrombolytic activity; anti-inflammatory activity; cadherin; tumour invasion suppressor activity; tumour inhibition activity; di
                                                                                                                                                         2102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted protein; immune stimulating;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV63196;
                                                                      1607
                                                                                                                                                                                                                                                                                Sequence 2522 BP; 740 A; 577 C; 637 G; 565 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 31; Pages 86-88; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adult brain, adult blood and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide(s) and secreted proteins from human cDNA libraries prepared from adult testes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-542703/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-1998;
28-MAR-1997;
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                                        gaaaaattmaaagacaaggctggttacatgtctgggatgctggtgcctgtaggggttggg
                                                        gaaaaaagaaaagaactggaagtgtgcatcacacagttgctcatccagctgggaatttga
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A, Spaulding
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97US-0823330
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47.4%;
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Treacy M;
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    are obtained
foetal brain,

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Db 2282 atagctggagccttgttcatcttgggagccctctacagcattaaggttatga 2333

Search completed: September 16, 2002, 20:19:54 Job time: 12101  $\sec$ 

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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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       GenCore version Copyright (c) 1993 - 2000
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US-08-928-361B-3
US-08-967-974-2
US-08-968-8510-133A-32
US-08-685-895-32
US-08-99-811-3
US-08-99-811-3
US-08-99-811-1
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Compugen Ltd.
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(without alignments)
7540.089 Million cell updates/sec
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Sequence 14, Appl
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TILING DATE: ATTORNEY/AGENT I NAME: BENT, S REGISTRATION N REFERENCE/DOCK TELECOMMUNICATIO TELEPAN: (703 TELEFAX: (703 TELEFAX: (703 TELEFAX: 899149 INFORMATION FOR SE SEQUENCE CHARACT LENGTH: 7218 TYPE: nucleic STRANDEDNESS: STRANDENESS:	COUNTRY: ZIP: 2231 COMPUTER REA MEDIUM TYP MEDIUM TYP COMPUTER: OPERATING SOFTWARE: CURRENT APPL APPLICATIO FILING DAT CLASSIFICA PRIOR APPLICATIO APPLICATIO APPLICATIO APPLICATIO APPLICATION FILING DAT FILING DAT FILING DAT	SULT 1  -08-232-463-14/c  Sequence 14, Applica Patent No. 5670367  GENERAL INFORMATION APPLICANT: DORNE APPLICANT: FALKN TITLE OF INVENTION NUMBER OF SEQUENC CORRESPONDENCE AD ADDRESSEE: FOLSTREET: ALEXANDER STATE: VA		
FILING DATE: 25-AUG-1991 ATTORNEY/AGENT IMPORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 300 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300 TELEFAX: (703)83-4109 TELEFAX: (703)83-4109 TELEFAX: 899149 TELEX: 899149 TELES: 899149 TELES: 899149 TELES: SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE: CLONE: pTZ9pt-F1s CLONE: pTZ9pt-F1s -232-463-14	USA IBI SYST SYST ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT ICAT IC	-14/c , APPlicatio 5670367 FORMATION: T: BOREFELI T: SCHEIFLI T: FALKNER, INVENTION: F SEQUENCES: NDENCE ADDRE SEE: FOLEY ALEXANDERIA VA		
26-AUG-1991 26-AUG-1991 SIENDER: 29 NUMBER: 29 NIVABER: 29 NI INFORMATION: KET NUMBER: 20 NI INFORMATION ON INF	299 LE FORM: Floppy disk Floppy disk M PC compatible FEM: PC-DOS/M TEM: PC-DOS/M TEMIN PC-DOS/M TON DATA: US/08/ US/08/ US/08/ US/07/ U	9 0 0	1361 2885 2885 2885 2885 2885 2885 2885 1644 1104 1104 1360	11385 405 405 1361 1361 1361
11991 110N: A. 29, 29, 29, 29, 29, 29, 29, 20, 11rs	is)	rdr Rc	44444WW4W4	22444
1 1 768 30472/114 ION: 0 0	k ible S/MS-DC s/e #1. 08/232, 07/935,	n US/08232463 F. R. G. RECOMBINANT FOWLPOX VIRUS S2 S5 Lardner Lardner onal Road, Suite 500	US-09-232-201-20 US-09-232-200-36 US-09-232-200-56 US-09-232-197-56 US-09-232-197-56 US-09-232-201-36 US-09-32-201-56 US-08-781-891-208 US-08-781-891-208 US-08-781-891-208 US-09-431-500A-1 US-09-431-500A-2 US-09-431-500A-2	044-908- 299-074F 399-773- 232-191- 232-200- 232-197-
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                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Perry III, William L.
APPLICANT: SKOINICK, MARK H.
TITLE OF INVENTION: SPECIFIC MUTAT
TITLE OF INVENTION: SUPPRESSOR IN
NUMBER OF INVENTION: SUPPRESSOR IN
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICATION NUMBER: US 08/782,482
FILING DATE: 10-JAN-1997
                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPATING SYSTEM: PC-DOS/MS-DOS

COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Teng, David H-F.
APPLICANT: Tavtigian, Sean V.
                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               CITY: Washington STATE: DC
                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, N.W., Suite 1000
                 NAME: Saxe, Stephen A. REGISTRATION NUMBER: 3
                                                                                                                                        FILING DATE:
                                                                                                                                                       APPLICATION NUMBER:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            catggatattcctgttagcaaccatacagtgggagaagatgggttaaaatcaagtaagaa 1541
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                                                                                                                                                                                                                                                                                            U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIFIC MUTATIONS OF MAP KINASE KINASE
4 (MKK4) IN HUMAN TUMOR CELL LINES IDENTIFY IT AS A TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                    SUPPRESSOR IN VARIOUS TYPES
                                                                                                                                                          US/08/874,186
                 38,609
 24884-121392-01
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Best Local
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                         279
     tgttgggacgaactgtatgcttgctcgtggtggaactggtgctgtagcgccagtgttgga 338
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; NAME/KEY: CDS
; LOCATION: (1)..(2190)
US-09-625-188-19
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                                                                                                                                                                                                               SEQ ID NO 19
LENGTH: 2190
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/09625188 Patent No. 6307037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-952-050: 10 INFORMATION FOR SEQ ID NO: 40: SEQUENCE CHARACTERISTICS: LENGTH: 2167 base pairs
                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/625,188
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                         SENERAL INFORMATION:
APPLICANT: NO. 6307037artis AG
TITLE OF INVENTION: Fungal Tarx
FILE REFERENCE: PB/5-31285P1
                                                                                                                                                                                   ORGANISM: Ashbya gossypii FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
TELEFAX: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3610 ttttgttttgccagtccaagaaacgtcctcctgttacttttgtagttgtactcatactagt 3669
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1574 TGTTGTTGTGGTTGCTGTTGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC 1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 TATTGTATTTCCATTTTAAGTAAAGGCAAGGTGATATTTAAGATGTATAAGAATAACAGA 230
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                 tctcctcgtcgttggtgatcgatatggagattgttgcagtagatcaggaggaggtagttcgtgt 278
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Similarity 54.7%;
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51.8%;
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                                                                           Score 37.6; DB Pred. No. 0.33;
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                                                               Mismatches
                                                                                            DB 4;
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: SEQ ID NO 1

: LENGTH: 5163

: TYPE: DNA

: ORGANISM: Cryptosporidium parvum

US-08-700-651-1
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; Sequence 4, Application US/08928361B

; Patent No. 6071518
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Best Local S
Matches 122
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APPLICANT: SUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORTICUM
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILLING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILLING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
ANDIBER OF SEQ ID NOS: 15
NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LEECH, JAMES APPLICANT: NELSON, RICHARD, C.
                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1454 AGAGACTGTTGCTGCTGCTGCTGCTGCTGCTGGAGGTGGTG 1411
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nes 122; Conserv
                    STREET:
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   Palo Alto
                 385 Sherman Avenue,
                                                                                                                                                 Petersen,
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PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
SPECIES INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37.4; DB Pred. No. 0.72; 0; Mismatches
                 JONES & BIKSA
e, Suite 6
                                                                                                                                                                                                                                                                                  780
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          Sequence 2, Application US/08700651B
Patent No. 6015882
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: RELSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PRO
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREAT
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
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Best Local
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
EARLIER APPLICATION NUMBER:
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APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "."
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CLASSIFICATION:
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Local Similarity 46.48;
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DEDNESS: double
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                                                                                AND TREATMENT
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                                                                                               PROTEINS,
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GLYCOPROTEINS,

Cryptosporidium

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US-08-928-361B-3/c
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LENGTH: 5318
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Best Local
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Patent No. 607
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NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Peterser
TITLE OF INVENTION:
TITLE OF INVENTION:
TELEFAX: 650-324-1678 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                 ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                     REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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CITY: P
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Local Similarity 46.4%;
nes 122; Conservative
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                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 12-SEP-1997 CLASSIFICATION:
                                   TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                            385 Sherman Avenue,
                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Petersen,
                                                                                                                                                                                                                                                                                                                                                                                                                           PETERS, VERNY, JONES & BIKSA
S Sherman Avenue, Suite 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS, THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carolyn
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Pred. No. 0.74;
0; Mismatches 141;
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; TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic) US-08-928-361B-3
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US-08-676-967-2
; MOLECULE TYPE:
US-08-676-967-2
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Best Local Similarity
Matches 122; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                     TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 5318 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
COERMANDED: PATEBLE PC-DOS/MS-DOS
                                                                                                                                REFERENCE/DOCKET NUMBER: UC TELECOMMUNICATION INFORMATION: TELEPHONE: (415)343-4341
                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
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STATE: CA
                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 530
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                                         STRANDEDNESS:
                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                            TOPOLOGY:
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US-08-676-974-2
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                                                   TELEFAX: (415)... 2:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
FRIGTH: 2277 base pairs
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Best Local Similarity
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APPLICANT: COLLINS, KATHLEEN
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                                                                                                           REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEPHONE: (415)343-4342
NFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
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MOLECULE TYPE:
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CLASSIFICATION:
                               STRANDEDNESS: double
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268 Bush Street, Suite 3200
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Best Local Similarity
Matches 116; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: COLLINS.
TITLE OF INVENTION:
                                                                        TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: OSMAN Ph.D., RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCBS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Science & Technology Law STREET: 268 Bush Street, Suite 3200
                 STRANDEDNESS:
                                                         LENGTH:
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US-08-510-133A-32
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Best Local Similarity
Matches 116; Conserv
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GENERAL INFORMATION:
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              INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                749
                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,133A
PILING DATE: 01-Aug-1995
CLASSIFICATION: CURSUIT LING DATE: 01-Aug-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/32863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             accaaagatcctaacccaatgtctggaaaggaacgtgatcaggttgctgagcagtgcaat 1146
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshal
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Joukov, Vladomir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Receptor Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgtgaagaagttgttctcaaaagaagctccaaatctaagaggaagacggataagaagttg 1266
                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARGAYGARGARGARAAYATHGARWSNAA 779
                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 Sears Tower,
                                                                            TELEFAX: 312/474-0448
LENGTH: 1140 base pairs
                                                     TELEX: 25-3856
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30 Sears Tower, 233 South Wacker Drive
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IOCATION: 37..1089
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-08-510-133A-32
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Best Local
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                                                                                                                                       TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Joukov, Vladimir TITLE OF INVENTION: Receptor
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CURRENT APPLICATION DATA:
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                                              MOLECULE TYPE:
                                                                                                                          SEQUENCE CHARACTERISTICS:
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                               FEATURE:
                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                             STRANDEDNESS: SI
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                                                                                                                                                                                                                                      REGISTRATION NUMBER:
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LOCATION:
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                  NAME/KEY:
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                                                                                         nucleic acid
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6300 Sears Tower, 233 South Wacker Drive
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                                                                                                           1140 base pairs
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 CDS
37..1089
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                                              DNA (genomic)
                                                                             single
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FEATURE:
NAME/KEY:

mat_peptide

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US-08-585-895-32
RESULT 14
US-08-999-811-3
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Best Local Similarity 53.1%;
Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                              Query Match
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APPLICANT: Rosen, Craig A.
APPLICANT: Cao, Liang
APPLICANT: Cao, Liang
APPLICANT: Cao, Liang
TITLE OF INVENTION: Polynucelotides Encoding Vascular Endothelial Growth
TITLE OF INVENTION: Factor 2
FILE REFERENCE: PF112D1
CURRENT APPLICATION NUMBER: US/08/824,996B
CURRENT FILING DATE: 1997-03-78
EARLIER APPLICATION NUMBER: 08/207,550
EARLIER FILING DATE: 1994-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                            PEATURE: mat_peptide LOCATION: (143)..(1120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: sig_peptide
LOCATION: (71)..(142)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (71)..(1120)
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                                                                   981 gaaagaagttccaccaccaaacatg 1005
                                                                                                                                                                                                                                                                            / Match 0.9%;
Local Similarity 53.1%;
les 77; Conservative
                                                                                      tatggtggtgaaagcaccagaaatg 1885
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                                                                                                                                                                                                                                                                          ; Score 36.2; DE; Pred. No. 0.7; 0; Mismatches
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US-08-999-811-3
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Best Local Similarity 53.1
Matches 77; Conservative
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APPLICANT: HU, JING-SH
APPLICANT: ROSEN, CRAI
APPLICANT: CAO, LIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202)371-2540 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                      FEATURE:
                         1861 tatggtggtgaaagcaccagaaatg 1885
                                                                                              1801
                                                                                                                                               1741 aatatgcataagacagatgtctgtcagcatgtatcagaaatctccacacagaggtgctca 1800
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APPLICATION NUMBER: US 0:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US
FILING DATE: 8-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1526 base pairs
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                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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981 GAAAGAAGTTCCACCACCAAACATG 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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ZIP: 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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                                                              TAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAG
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ROSEN, CRAIG A.
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RESULT 15 US-09-042-105-3

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Sequence 3, Application US/09042105
Patent No. 6040157
GENERAL INFORMATION:
APPLICANT: HJ, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                     LOCATION:
US-09-042-105-3
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NAME: ERIC K. STEFFE
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEPHONE: (202)371-2540
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1526 base pairs
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Best Local Similarity 53.1%;
Matches 77; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
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APPLICATION NUMBER: TO BE ASSIGNED FILING DATE: 24-DEC-1997
CLASSIFICATION:
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PRIOR APPLICATION UNMER: US 08/465,968
APPLICATION UNMER: US 08/465,968
FILING DATE: 06-JUN-1995
                                                                             1741 aatatgcataagacagatgtctgtcagcatgtatcagaaatctccacacagaggtgctca 1800
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1801 tcaaaggggaaaacagcgggtttgagtaaggggaaaacacattcagctgctagtaccaaa 1860
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ZIP: 20005
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STREET: 1100 NEW YORK AVENUE
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                                                        861 AATTTGATGAAAACACATGCCAGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCCC 920
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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LOCATION:
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Pred. No. 0.7;
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В 981 GAAAGAAGTTCCACCACCAAACATG 1005

Search completed: September 16, 2002, 20:09:49 Job time: 11506 sec

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Copyright (c) 1993 - 2000 Compugen
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13360.877 Million cell updates
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-	BE427089 PSR6397 I	A2550256 ENTEV58TR	BE427548 PSR7168 I	BE427036 PSR6610 I	AL191328 Tetraodon	AL415192 T3 end of	AW187871 BNLGH1134	AZ031624 RPCI-23-2	C93179 C93179 Dict	AW727582 GAEa001	Ů,			AL072375 Drosophil	BG845969 1024011G0	AL108707 Drosophil	BF242104 601879787	BH156851 ENTQY92TR	AL066834 Drosophil	AL109275 Drosophil		AI641313 fc13d05.y	AU060996 AU060996			AG126399 Pan trogl	AQ584620 RPCI-11-4

## ALIGNMENTS

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KEYWORDS
SOURCE
ORGANISM
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TITLE
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606020C11.x1 606 - Ear tissue ci
mays cDNA, mRNA sequence.
A1691520
A1691520.1 GI:4966664
EST.
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Zea mays
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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                 Email: walbot@stanford.edu
Plate: 606020 row: C column:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
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/db_xref="taxon:4577"
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ear tissue cDNA library from Sc
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                                  33 gttqttctagcgtgtgcagcggctagctgattgattgtcttctgtgatatatccagagct 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTATGGTACGGGTCAGCCTTCGACCAGTGGCAATGGGAGGACCATTCATCCGTTGGATA 244
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CNS0071A 895 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR14809 of RPCI-98 library from Drosophila melanogaster (fruit
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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                                            1004 aactttctgaagtggtcctcaaaagaaatgaagatgaaaatggaaaaatggaaaaactgaagagactc 1063
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         - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                fly), genomic survey sequence. AL066784
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Pterygota;
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 and how to order individual BAC clones,
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arygota; Neoptera; Endopterygota; Diptera; Brachycera;
scomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                           Drosophila melanogaster genome survey sequence T7 end of E
BACN16J16 of DrosBAC library from Drosophila melanogaster
fly), genomic survey sequence.
AL106910
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                                                                                                                                                    Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
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/db_xref = "taxon:7227"
/clone_lib "RPCI-98"
/clone="BACR14D09"
/note="end:TET3"
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/organism="Drosophila melanogaster"

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AL065073
Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and aaron Mammoser in Pieter de Jong's laboratory in the Department of
                                                                                                                                                                                                       Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins.
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 884)
                                                                                                                                Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                     Direct Submission
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/clone_lib="DrosBAC"
/clone="BACN16J16"
/note="end: T7"
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- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part o Determination with the Berkeley Drosophila Genome Project (BDGP) rocollaboration with the Berkeley Drosophila Genome Prosophila The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information melanogaster secone using these BACs. For further information please see http://www.fruitfly.org The BDCP Drosophila please see http://www.fruitfly.org The BDCP Drosophila please see http://www.fruitfly.org The BDCP Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
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pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14N21"
/note="end : T7"
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Drosophila melanogaster genome sur
BACR27J03 of RPCI-98 library from
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/db_xref-"taxon:7227"
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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AL060767.1 GI:4943573
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Genoscope.
Direct Submission
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16; Mismatches 248;
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- Web: www.genoscope.Cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Patetr de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                      Drosophila melanogaster genome sur
BACR39G08 of RPCI-98 library from
fly), genomic survey sequence.
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AL076720
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACRL2K22"
/note="end : TET3"
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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       Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37G05 of DrosBAC library from Drosophila melanogaster (from Drosophila melanogaster)
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/db_xref="taxon:7227"
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 985)
                                      Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
                                                                                                                  Eukaryota; Metazoā; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fly), genomic survey sequence AL108478
- Web : www.genoscope.cns.fr) 
 Determination of this BAC-end sequence was carried out as part of
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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/clone="BACN37G05"
/note="end : SP6"
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Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail :
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/db_xref="taxon:7227"
/clone_lib="RPCI-88"
/clone="BACR32D23"
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Determination of this BAC-end sequence was carried out as part of a Determination with the European Drosophila Genome Project (EDGP) - Collaboration with the European Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Watson, B.S., Shin, H.-S., Lopez-Meyer, M., Scott, A.D., Harris, A.R. Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., G.D. and Paiva, N.L.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
OK Noble Parkway, Ardmore, OK
                                                                            Medicago truncatula nodulated Unpublished (2000) Contact: Paiva NL
                                                                                                                                                                                                                     Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                            AW684844 706 bp
NF022B10NR1F1000 Nodulated root
                              2510
                                                                                                                                                                                                                                                                                                                  AW684844.1 GI:7559580
                                                                                                                                                                                                                                                                                                                                            NF022B10NR 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                        Medicago.
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580 221 7317
580 221 7380
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/clone="BACN37L10"
/note="end : T7"
a 177 c 105 g
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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Pred. No. 1.3;
39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               706 bp
                                                                                                              root
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                                     73402, USA
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                                                                                                                                                                            Harris, A.R.,
                                                                                                                              Foundation
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                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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Best Local
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Plate:
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                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
BI176637
BI176637.1 GI:14642448
                                                                                                                                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                                          Baker,B
                                                                                                                                                                                                                                                                                                                                                                      Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                    potato.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.2%;
Similarity 50.9%;
09; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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022 row: B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nlpaiva@noble.org
Length: 706 Std Error:
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                                                    /db_xref="taxon:4113"
/clone="cSTE5K22"
         /tissue_type="axillary buds of stem explants;
sink-tubers"
                                                                                                                              Location/Qualifiers
                                        /clone_lib="cSTE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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997 actccaaaactttctgaagtggtcctcaaaagaaatgaagatgaaaatggaaaaactgaa 1056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTGAAAAGACTACTGAGAAAGAGATCAGTGATGATGAAGATGATGAGCCCCAAGAAGGAA 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Cathy Ronning
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 748)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI176637 748 bp mRNA linear I
EST517582 cSTE Solanum tuberosum cDNA clone cSTE5K22
                                                                                       For clone info: please contact Research Genetics, pivision tel 1-800-711-6195, email cdna@resgen.com Seq primer: M13F-R.
                                                                                                                                                                                                          Generation of ESTs from in vitro grown microtubers Unpublished (2001)
                                                                                                                                                                                                                                                                               van der Hoeven,R., Bezzerides,J., Bachem,C., Viss
Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: Lambda Zap; Four-week old Rhizobium meliloti-inoculated Medicago truncatula roots, confa mixture of young and old roots and nodules."

119 c 175 g 168 t 4 others
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/db_xref="taxon:3880"
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/dev_stage="Pooled developmental"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="NF022B10NR"
/clone_lib="Nodulated root"
/organism="Solanum tuberosum"
/cultivar="Bintje"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB (
Pred. No. 1.2;
0; Mismatches
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                                                                                                                                                                                                                                                                                        Visser,R., Cho,
,C., Tanksley,S.
                                                                                                                                                  Libraries
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2 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUL-2001
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BASE COUNT
ORIGIN
Search completed: September 16, 2002, 18:12:16 Job time: 9974 sec
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                                                                                                                                                                277 TGATGAGGATCACCAC 262
                                                                                                                                                                                                             387 cgaaccggcacaacac 402
                                                                                                                                                                                                                                                                                                    337 TGGAATTGTTGCTGTGGCAGCGGCGGGTGCTGGTGCTGGTGCTGCTGCTGCTGCTGC 278
                                                                                                                                                                                                                                                                                                                                    327 gccagtgttggagctgacagcgacgcctcgtcaggatgcagccgctgaagctggtgtaga 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 gggagctcgtgttgttgggacgaactgtatgcttgctcgtggtggaactggtgctgtagc 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 gtgtttgattctctcctcgtcgtggtgatcgatatggagattgtttgcagtagatcagga 266
                                                                                                                                                                                                                                                                                                                                                                                                                                     208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Wector: pBluescript SK(-); Site_1: EcoRI; Site_2: Anote="Wector: pBluescript SK(-); Site_1: EcoRI; Site_2: Anote="Wector: pBluescript SK(-); Site_1: EcoRI; Site_2: Anote="Wector: pBluescript Skip: plant Breeding, Wageningen University, The Netherlands). The cSTA libraries will attempt to capture the induction and initiation/initial growth of the tuber in an in vitro system as described in Bachem et al. (Plant Journal, 1996). Small microtubers develop from axillary buds attached to stem explants when placed on a high sucrose medium (10%). Visible morphological changes occur synchronously at day five in the axillary buds harvested on days 1-3. This targets of axillary buds harvested on days 1-3. This targets those genes involved in induction of the microtubers. The following libraries, CSTA (21-40) and CSTA (41-60), capture genes involved in tuber initiation and outgrowth. This library is noted as P3 in Tanksley lab notebooks."
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/lab_host="SOLR"
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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                           Score
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb;
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_vtrus:*
13: sp_verteb;
13: sp_verteb;
14: sp_unclass:
15: sp_archeap;
16: sp_bacteria:
16: sp_archeap
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## RESULT OPENICATION Ş В Ş В δÃ Query Match 100.0%; Best Local Similarity 100.0%; Matches 1057; Conservative 0; STRAIN-CV. NIPPONBARE; Sasaki T., Matsumoto T., Yamamoto K.; Sasaki T., Matsumoto T., Yamamoto K.; Poryza sativa nipponbare(GA3) genomic DNA, chromosome 1, clone:P0485D09."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP001859; BAA94774.1; -. Hypothetical protein. SEQUENCE 1385 AA; 151678 MW; 16E784264EEFC7B5 CRC64; HYPOTHETICAL PROTEIN. Oryza sativa (Rice). Oryza sativa (Rice). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Spermatroideae; Oryzeae; Oryza. O91ML4 PRELIMINARY; PRT; 1385 AA. O91ML4; O1-DCT-2000 (TrEMBLrel. 15, Created) O1-OCT-2000 (TrEMBLrel. 15, Last sequence update) O1-DEC-2001 (TrEMBLrel. 19, Last annotation updat SEQUENCE FROM N.A. NCBI_TaxID=4530; 121 329 61 GTAPRTLPAKQNGTSDGCSITFVRSTFVPASVGSQKVSPSTQSSQGKNADRSTLPKSVQE IRGYVALLQKKDPKFCSLSRIFHDQKKCDEHKASSSPFSVAKFRRWDCSKCLDKLKTSDN 120 IRGYVALLQKKDPKFCSLSRIFHDQKKCDEHKASSSPFSVAKFRRWDCSKCLDKLKTSDN 448 0; Score 5526; Pred. No. 0; 0; Mismatches DB 10; update) 0; Indels Length 1385; 0; Gaps 388 60

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EU Arabidopsis sequencing project;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEEMVTIAASSPLFSHHDDQYIAEAPTEHWGRKDAKKLTWEQFKATTRNSPAATCGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNSQQ--KSLASQSTQKELQGHLALTTQESPH------PQN---FQSTQEQQTHLR |: : | : | | | | | | | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDIPMDIVELLAKNQHERQLM-TETDCSDINRIQSKTTADDDCVIVAAKDGSDYASSVFD
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DKEKKQKRKAESCNNNASAGPVKNSSGPIVCSVNRNPADFTIPEPGNVYM
                                   DRFVRQD----
                                                                         RKDT----FAPVYNTHEKPVFASSNDQAKFQLLGASNS-
                                                                                                                                                                                  SRHQLHDLHRPLRP-HPRVGVLGSLLQKEIANWSENCGTQSGYKLGVSTGITSHQMNRKE
                                                                                                                                                                                                                                                                                                  NENTWNLNFVAANGKQKCGPNPEFSFGCKHAAGVSSSSSRPIDNFSSESSIPALHLLSLL
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                                                                                                             HFEALNSGMFSAKWNALQLGSVSSSAD-----FLSARNSIAQSWTRGKGKMVHPL----
                                                                                                                                                     SKRFTQEPSRKSFPITPPIGT--SSLSFQNASWSPH-------HQEKKTK
                                                                                                                                                                                                                                DPRLRSTTPADQHGNTKFTKRHFPPANQSKEFIELQTGDSSKSAYSTK---QIP--FDLY
                                                                                                                                                                                                                                                                DPSTLASFP--NYGTS--SRNOMESQLHNSQYAHNQYKGSTSTSYGSNLNGKIPLTFEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ASSIRFSGHNCQWLGNLPTV--GNQNPSPSSFRVLRA-----CDTCQSVPN
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Best Local Similarity
Matches 210; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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KIAA0624.
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TISSUE-BRAIN;
                                                                                                                                                                                                                                                   1334 LAPTLQEMASVEAAVSLPEEESKAREIFSDNLAKTPLGDSENKKER------
                                                                                                                                                                                                                                                                                                                                                                                       1219 TLHKVK-TTSTFSVSGDE----DNVKCLEVVSIYYTLPRKPSKKFCNLLQQYTQNTNLLI 1273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNNVEDAMGNYMLNKFSPSSPESANECSKVLSDSA---LEAPEATERMTNVKSSGSTSVR 1105
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               MIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSDY-----
                                                                                                                                                                                   ---GKKLQSETLHTSLMLQRKNVSEEK-SENCQQSINSSNSGPSSLPA-LSEVNIGNSQT
                                                                                                                                                                                                                                                                       CEDD------RSTIPVPMEVSMDIPVSNHTVGEDGLKSSKNKTKRKYSDVVDDGSSLMN 452
                                                                                                                                                                                                                                                                                                                      ESPQYETETFPNALEKDKQNYSTREQSGTPSCENLKMSVNSDQTLTTENMTAFRLSNRGP
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                                                                                                                                                                                                                                                                                                                                                                                                                     VAEQCNLTKDPKPVSGQKCEQICNEPCEEVVLKRSSKSKRKTDKKLMKKQQHSKK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITFVRSTFVPASVGSQKVS------PSTQSS---QGKNADRSTLPKSVQEG-----
                                               - NKTLSHSESQVFALTPALHKLQLGEETQSDEPNLESLQSEPRELPQRSQEANMTESRK-\\
                                                                                                                RRSSWECTGSGRAIPFTGSGKCPQKDHTSTAVGDGSSGSQPREGRG----DIGTNCQKMT
                                                                                                                                               EISTORCSSKGKT-----AGLSKGKTHSAASTKYG--GESTRNGONIHVLSAEDOCOMET 565
                                                                                                                                                                                                                      WLNGKKKRTGSVHHTVAHPAGNLSNKKVTPTASTQHDDENDTENGLDTNMHKTDVCQHVS
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                                                                                ENSVLSHSAK----VSPAEHDIQIMSDLHE-----QSLPKK--KKKQKLEVTREKQT
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Pred. No. 6.2e-05;
71; Mismatches 42:
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	•	834 YOSVEAKEKNENGGYDTNYGNKEDSKDLKDDRSVEVKANKEESMKKKREEVQRNDK	Db	
	РP	VPQITWHIEVNGADO	Qy	
	DKEESKD 833	KSVETKDNKKLSSTENRDEAKERSGEDNKE	Db	
	3PMKD 206	SQKVSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAEANTDS	Оу	
26	; Gaps	Query Match 3.9%; Score 216; DB 10; Length 2081; Best Local Similarity 18.9%; Pred. No. 0.00013; Matches 155; Conservative 139; Mismatches 382; Indels 144	Z W O	
		Res. L; AF UENCE	RL DR SQ	
	inety P1,	Arabidopsis thaliana chromosome 3. II regions of 4,251,695 bp covered by n	RRR	
		SEQUENCE FROM N.A. STRAIN-COLUMBIA; MEDLINE-20363099; PubMed-10907853; Nakamura Y.;	R R R R	
	;	100) to the EMBL/GenBank/DDBJ databases.	RL	
	n	י איניייייייייייייייייייייייייייייייייי	RCR	
	;	sicales; Brassicaceae; Arabidopsis.	200	
	hyta; Rosidae;	ridiplantae; Streptophyta; Embryophyta; Tracheop . Marmoliophyta: endicotyledons: core endicots:	888	
		01-DEC-2001 (TremBLrel. 19, Last annotation update) GENOMIC DNA, CHROMOSOME 3, BAC CLONE: T19N8.	DE DI	
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	FSAK 989	930 RPHPRVGVLGSLLOKEIANWSENCGTQSGYKLGVSTGITSHQMNRKEHFEALNSGMFSAK	ΟV	
	F)	95 NVHGDLLRKS	B 5	
	HRPL 929	870 PNYGTSSRNOMESOI	Q	
	LASE 869	810 YABRAVNQVHARNEPSTIAIMEASKICDRRNAGOVVIPKESMPATHILIKMUDSTLAS	Db Qy	
	EP 17	LVRESGAPSPITFTSLREAEFSDNQRRLSPPF-	Db	
	00	THVMGSSSNYASRQPVIA	Qy	
	KHENS 1710	1651 SRLSENRKHVKKSENLLPITVLPNREPSTHVSNQKSNSISQRHQNEFKNVSESPSKI	Дb	
	1WGR 749	EIAEAPT	Qy	
	SIGE 1650		Db	
	3 708	ric.	Qy	
	RLA 1590	1549AEDEMQKSAWDQPSLPEGNKNKTNLDDLVKGENRSSVKHRLA	DЬ	

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RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Amendar J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
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01-NOV-1996 (TrEMBLTel. (
01-DEC-2001 (TrEMBLTel. 1
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                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
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ZK783.1.
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Caenorhabditis.
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Best Local Similarity
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STRAIN-BRISTOL N2;
STRAIN-BRISTOL N2;
Favello A., Vaudin M.;
Favello C. elegans (
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00010; ASX_HYDROXYL; 9.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS001186; EGF_2; 22.
PROSITE; PS01187; EGF_CA; 13.
PROSITE; PS00135; TRYPSIN_ESE; UNKNOWN_1.
Calcium-bhdding; EGF-1ike domain; Glycoprotein; Hydroxylation; SEQUENCE 3507 AA; 365315 MW; 154F0B687874D9DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston F Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III elegans";
 2183
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[2]
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                                                                                                                                                                                             SSNSGQEKPTTKGIVSSTSATSSESTTAEPHVTTSISSTTSTKDMTSSKSPENVTMSSES
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 PVKLSSLSPDVSQPSTKTFDATESSTVQASETSSGTSVKSTSEPESHVTKLSITSSNPSS
                       PVSGQKCEQICNEP-----
                                                SSEAPVTSTSPTEVHTSSETKPSLSASSTTGDTNSTTPSTSSLASVKSTSAPEGTSASVA
                                                                                               TTPKEESSSEITVKLSSKSPEVT----
                                                                                                                                             PEVSTSSSKSTTASETTVSSTPSESSSSEAPLTSSPATTTEVITESSVKS---
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                                                                                                                      AANVSEDNTSVDVGALPEVPQITWHIEVNGADQPPSTPKLSEVVLKRNEDENGKTEETLV
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IPR001881;
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IPR001507;
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EGF-like.
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                       -CEEVVLKRSSKSKRKTDKKLMKKQQHSKKRTAQADVSDA
                                                                      --DPNPMSGKERDQVAEQCNL----
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EMBL/GenBank/DDBJ
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Pred. No. 0.0
                                                                                               ESSVKSSPSTPSTTSQSVTSTVPETSKS--TVL
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044929;
01.JUN-1998 (TrEMBLrel. 06, Created)
01.JUN-1998 (TrEMBLrel. 06, Last sequence update)
01.JUN-2001 (TrEMBLrel. 17, Last annotation update)
10.JUN-2001 (TrEMBLREL PROTEIN D-CLIP-190.
CLIP-190 OR CG5020.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapo
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                                                                                                                                                                              RSCECDAGYIGDGYVCSPHPQDCVLRDNLC
                                                                                                                                                                                                                                   TVTCHSLATCEQ----STGVCICRDGFIGDGTTACSKKSTADCISLPSLCADKAKCDNST
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                                                                                                                                                                                                                                                           GITSHOMNRKEHFEALNSGMFSAKWNALQLG----SVSSSADFLS----ARNSIAQSWT
                                                                                                                                                                                                         R-----GKGKMV--HPLDRFVRQDIC 1035
                                                                                                                                                                                                                                                                                                                                                                    -----AH-NOYKGSTSTSYGSNLNGKIPLTFEDLSRHQ-----
                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                   -LHDLHRPLRPHPRVGVLGSLLQKEIANWSENCGTQSGYKLGVST
                                                                                                                PRT;
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         Insecta;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SERJUNCE FROM N.A.
STRAIN-OREGON R;
Lantz V.A., Miller K.G.;
Lantz V.A., Miller K.G.;
J. Cell Biol. 0:0-0(1998).
J. Cell Biol. 0:0-0(1998).
EMBL; AF041382; AAB96783.1; -.
FiyBase; FB9000338; CAP-GLY; -2.
Pfam; PF01302; CAP-GLY; -2.
SEQUENCE 1690 AA; 189103 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQKNINELKARIVELESALGNERK-----KTEELQCSIDEAQFCGDELNAQSQVYKEKI 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                          OHVSEISTORCSSKGKTAGLSKGKTHSAAS-TKYGGESTRNGQNIHVLSAEDOCOMETEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLMNWLNGKKKRTGSVHHTVAHPAGNLSNKKVTPTASTQHDDENDTENGLDTNWHKTDVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECGIENLRELALLKEENEKQAQEAQAEFT-RKLAEKSVEVLRLSSELQNLKATSDSLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSSKSKRKTDKKLMKKOQHSKKRTAQADVSDAKLCRRKPKKVRLLSEIINANQVEDSRSD 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALDDMLRLQKEGT-----EEKSTLLEKTEKELVQIKEQAAKTLQDKEQLE
                                                                                                                                                                                         MVTIAASSPLFSHHDDQYIAEAPTEHWGRKDAKKLTWEQFKATTRNSPAATCGAQFRPGI 780
                                                                                                                                                                                                                                      QKSLASQSTQKELQGHLALTTQESPHPQNFQ------STQEQQTHLRMEE
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                                                                                                                          QAVDLTSTHVMGSSSNYASROPVIAPLDRYAERAVNQVHA-----RNFPSTIATMEASKL
                                                                                                                                                                                                                         LKSQA-EETQSELK-----STESNLEAKSKQLEAANGSLEEEAKKSGQLQEQITKLKSEV
                                                                                                                                                                                                                                                                                      EQELQQLQSKSAESESALKVVQV-QLEQLQQQAAA-----SGEEGSKTVAKLHDEISQ
                                                                                                                                                                                                                                                                                                                    PMDIVELLAKNOHEROLMTETDCSDINRIQSKTTADDDCVIVAAKDGSDYASSVFDTNSQ
GSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPLRPHPRVGVLGSLLQKEIA-----NWS 950
                                                           CDRRNAGQVVLYPKESMPATHLLRMMDPSTLASFPNYGTSSRNQMESQLHNSQYAHNQYK 895
                                                                                           SDEIATGHKELTSKADAWSQEMLQK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE4F48FD15F17A7C CRC64;
                                    ----EKELQELRQQLQDSQDSQTKLK 1043
                                                                                                                                                                  ----VESKTKQLEAANAALE----
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Best Local 9
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EMBL; AL161579; CAB799;
Hypothetical protein.
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OPRELIMINARY; PRT; 852 AA.
O9SZ55;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 92.0 KDA PROTEIN.
F11C18 80 OR AT4G31880.
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Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck
De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R.
Gielen J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bevan M., Terryn N., Ardiles W., Buysshaert C., Da
De Clerck R., De Keyser A., Neyt P., Rouze P., Van
Villaroel R., Gielen J., Van Montagu M., Hoheisel
Mayer K.F.x., Schueller C.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AL049507; CAB40758.1; -
EMBL; AL161579; CAB79906.1; -
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                    DPKFCSLSRIFHDQKKCDEHKASSSPFSVAKFRRWDCSKCLDKLKT-----SDNGTAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILETVAKVRSCVVMLDLECDALLIEMFQHFLK--AIRDHHSGNVFSSMENIMTLVLEESE
                                                                                                                                                                                          CNAP---SGK----NGAAEAN-----TDSPMKD----LQGPAQNYDVAANVSEDNTSVDV
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  EVVLKRNE - -
                                                                                                         GALPEVPQITWHIE--
                                                                                                                                                         TDAPKDESGKSGVSNGVAQQNDSSVDTDSMKKQDDTGAKDEPQCLDNPRNTDLNNTT---
                                                                                                                                                                                                                                                                   PLDKYSNIVASICEGTF-----SALQQDQVVANEKEDSQGHIKRETEVEKAAEISTPER
                                                  --- EEKPDVEHQIEEKENESSSVKQADLSKDSDIKEETEPAELLDSKDVLTSPPVDSSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     opsis sequencing project; (APR-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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21.2%;
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DENGKTEETLVAEQCNLTKDPNPMSGKERDQVAEQCNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 209.5; DB Pred. No. 0.0001; 7; Mismatches 28
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T06E4.1 PROTEIN.
                                                                                                                     "Genome sequence of the nematode investigating biology."; Science 282:2012-2018(1998). EMBL; Z70756; CAA94789.1; SEQUENCE 1295 AA; 147395 MW;
                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                    T06E4.1.
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MEDLINE=99069613; PubMed=9851916;
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 VRSTFVPASVGSQKVSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNG----AAEA
                                          DQKKCDEHKASSSPFSVAKFRRWDCSKCLDKLKT-SDNGTAPRTLPAKQNGTSDGCSITF
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Viruses; dsDNA viruses, no RNA s
Betaherpesvirinae; Roseolovirus.
NCBI_TaxID=32604;
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with human herpesvirus 6A.";
virol. 73:8040-8052(1999).
EMBL; AF157706; AAD49674.1;
SEQUENCE 1520 AA; 171362 MW; 0F498E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TQKYKKTHIRCR-----SIQKTKGHSS--QTINKHKVQKHNEN--HVPS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTFVRSTFVPASVGSQKVSPSTQSSQGKNADRSTLPK-SVQEGNDSKCNAPSGKNGAAEA 198
                                                                                                                                                                                                                                                                                                                                 SGQKCEQICNEPCEEVVLKRSSKSKRKTDKKLMKKQQHSKKRTAQADVSDAKLCRRKPKK 370
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                                                                                                                                                                                                                               SSKNKTKRKYSDVVDDGSSLMNWLNGKKKRTGSVHHTVAHPAGN-LSNK-----KVTPT 483
                                                                                                                                                                                                                                                        ----SD--PSHNLHGKTSDEQYKTS-----PDNEKISTPPKSKTHHCIHDSSSSEEGQY 559
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                                                                         OCQMETENSVLSHSAKVSPAEHDIQIMSDLHEQSLPKKKKKQKLEVTREKQTMIDDIPMD
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                                                                                                                    EISTQRCSSKGKTAGLSKG------KTHS-----AASTKYGGESTRNGQNIHYLSAED
                                                                                                                                                      SKTNHKTEESTENTDLNSFSNENTNKTEIEDSNIIQPFSQLFCNETIIPSTSACPTQETP
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RASSRASSRASSRASSRTSSRASSRAFSRASSRVSSRASSRASSRASSRASSRASS
                        IVELLAKNQHERQLMTETDCSDINRIQSK--TTADDDCVIVAAKDGSDYASSVFDTNSQQ
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                                                    --CSSTENKSETSNQTNGENSDKPLSKTFTEVSDRASSRASSRASS
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pred. No. 0.00029;
70; Mismatches 480;
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              "Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; UB0022; AAC25885.2; -.
R InterPro; IPR001064; Crystallin.
R InterPro; IPR003962; FNIII repeat.
R InterPro; IPR003961; FNIII.
R InterPro; IPR003599; Ig.
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R InterPro; IPR003599; Ig.
R InterPro; IPR003598; Ig.-c2.
R InterPro; IPR003598; Ig.-c2.
R InterPro; IPR003598; Ig.-c2.
R InterPro; IPR003598; Ig.-c2.
R InterPro; IPR003006; Ig.-MHC.
R InterPro; IPR003006; Ig.-MHC.
R InterPro; IPR00130; Zn.-MTpeptdse.
R Pfam; PP00041; fn3; 7.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 385.7 KDA PROTEIN.
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STRAIN-BRISTOL N2;
Fulton B., Wohldmann P.;
"The sequence of C. elegi
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STRAIN-BRISTOL N2;
MEDLINE-99069613;
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Rhabditidae; Peloderinae;
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Best Local S
Matches 214
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SMART; SM00409; IG; 12.

SMART; SM00409; IG; 12.

SMART; SM00410; IG_11ke; 1.

PROSITE; PS00225; CRYSTALLIN BETAGAMMA; UNKNOWN_1.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.

Hypothetical protein; Immunoglobulin domain; Repeat.

Hypothetical protein; Immunoglobulin domain; Repeat.

SEQUENCE 3484 AA; 385746 MW; 21DD6F6893020F4F CRC64;
                                                                                                                                                   1009
                                                                                                                      543
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 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214;
                                                                                                                                                                                                         KKKIIKKKTEKSDSSISQKSATDSEKVSKQKEQDEPTKPAVSETQMVTEADKSKKQKETD
                                                                                                                                                                                                                                                                     KDEVTAEKQSTEALIESKKKEVDESKISEQQPSDKNKSEVVGVPEKAAGPETKKDVSEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IIKKKETPESEQVTAA---EPEQQKISEVDVQS-VAETEVGAKKKPDAEKPTDLSKAKKD
RQLMTETDCSDINRIQSKTTADD
                            GADAVKKQKELDEKNKLEANKKSAAGKLKIEEESAAKSKQTVEEQAKLD~AQTKAKTA-E
                                                         HEQSLPKKK - - - KKQKLEVTRE-
                                                                                        SADKLKLEEQAQAKKAAEVEAAKKQKEKDEQLKLDTEAASKKAAAEKLELEKQAQIKKAA
                                                                                                                     G-----ESTRNGQNIHVLSA-----EDQCQMETENSVLSHSAKVSPAEHDIQIMSDL
                                                                                                                                                     EKLKLDAEIAAKTKQEADEKSKLDAQEKIKKVSEDDAARKEKELN-DKLKLESEIATKKA
                                                                                                                                                                                TENGLDTNM-------HKTDVCOHVSEISTQRCSSKGKTAGLSKGKTHSAASTKYG
                                                                                                                                                                                                                                          KK-----KRTGSVHHTVAHPAGNLSNKK-------VTPTASTQHDDEND
                                                                                                                                                                                                                                                                                                     EVSMDIPVSNHTVGEDGLKSSKNK------
                                                                                                                                                                                                                                                                                                                                   DEQLKLETEVVSKKSAAEKLELEKQAQIKKAAEADAVKKQKELNEKNKLEAAKKSAADKL
                                                                                                                                                                                                                                                                                                                                                              PKKVRLLSEIINANQVED------SRSDEVHRE----NAADPCEDDRSTIPVPM
                                                                                                                                                                                                                                                                                                                                                                                              EAQKIAEVNKAKKQKEVDDNLKREAEVAAKKIADEKLKIEAEANIKKTNEVEAAKKQKEK
                                                                                                                                                                                                                                                                                                                                                                                                                          VVLK----RSSKSKRKTDKKLMKKQQHSKKRTAQ-----ADVSDAKLCRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLEKAADTTKQIETETVVDD----KSKKKVLKKKTEKSDSFISQKSETPPVVEPTKPAES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVP-QITWHIEVNGADQPPSTPKLSEVVLKRNEDENGKT-----EETLVAEQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 206; DB 5; Length 34:
Pred. No. 0.0011;
1; Mismatches 419; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -QGPA-QNYDVAANVSE----DNTSVDVGALP
                                                          KQTMIDDIPMDIVELLAKNQHE
                                                                                                                                                                                                                                                                                                       -TKRKYSDVVDDGSSLMNWLNG
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 -- DCVIVAAKDGSD
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                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-BRISTOL N2; Sun H., Geisel C.; "The sequence of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1417
                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 231.2 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Metazoa; Nematoda; Caenorhabditis.
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9N435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   751
                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                    Y38B5A.1
                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           900
                                                                                                                                       "Direct Submission.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC024760; AAF59460.2;
Interpro; IPR003962; FNIII_repeat.
Interpro; IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                   Submitted
                                                                     SMART; SM00060; FN3; 3
SMART; SM00409; IG; 3.
Hypothetical protein; 1
SEQUENCE 2083 AA; 2:
                                                                                                          PRINTS; PRO0014; ENTYPEIII
                                                                                                                      InterPro; IPR003599; Ig. Pfam; PF00041; fn3; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLKLDTEAASKKAAAEKLELEKQSHIKKAAEVD-AVKKQKELEEKQRLESEAATK---KA 1361
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 MEIVAVDQEGARVVGTNCMLARGGTGAVAPVLELTATP--
                      cal Similarity
175; Conser
                                                                                                                                                                                                                                  ence of C. elegans (MAR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      855
                                 3.7%;
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231174 MW;
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EMBL/GenBank/DDBJ
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                       Score 205.5; DB 5;
pred. No. 0.0006;
5; Mismatches 435;
                                                                           9270303ADE2D7C2F
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                             Indels
                                               Length
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RESULT 13
076891
1D 076891
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DT 01-NOV
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               076891;
01.NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EG:49E4 1 PROTEIN.
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 FUTSCH OR EG:49E4.1 OR CG3064.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RQDAAAEAGVDEPAQHQCEHFSIRGYVALLQKKDPKFCSLSRIFHDQKKCDEHKASSS-P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQCNLTKDPNPMSGKERDQVAEQCNLTKDPKPVSGQKCE-QICNEPCEEVVLKRSSKSKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLSHSAKVSPAEHDIQIMSDLHEQSLPKKKKKQKLEVTREKQTMID-----DIPMDIVEL 623
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                                                                                                                                                                                                                                                                                                                                                                               AEKOKLESEAATKKAAAEKLKLEEQAQINKAAEADAVKKOKELDEKNKLEANKKSAAEKL 1188
                                                                                                                                                                                                                                                                                                                                                                                                             LAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAK-----DGSDYASSVFDTNSQQK 678
                                                                                                                                                                                  ---PSESETQKVADAARKQKETDEKQKLEAEITAKKSADEKS
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                                                                                                                                                                                                                                                                                                                                         SLASOSTOKELOGHLALTTQESPHPONFOSTOEOOTHLRMEEMVTIAASSPLFSHHDDQY 738
                                                                                                    PRELIMINARY;
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Best Local
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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                                                                                                                                                                                  TPSAPEHISRADSPAECASEEIASQDKSPQVLKESSRPAWVAESKDDAAQLKSSVEDLRS
                                                                                                                                                                                                                                                       KLQTDSSPVDVAEGDFSHAVA-----SVSTVTPTLTKPAELAQIGAAKTVSSPLDEALR
                                                                                                                                                                                                                                                                                                                               AAVAIEDDAKSSISPKDKSRPGFVAETVSSPIEEATMEFSKIEVVEKSSLALSLQGGSGG
                                                                                                                                                                                                                                                                                                                                                                                                  LDKPQIIK-----DDKSTEHSRRESL----EDKSAVTSEKSVSRPLSVASDHE
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   INR---
                                     DVAHASVQPAELSKVDIEKTASSPIDEAPKSLIGSPAEERPESPAESAKDAAESVEKSKD
                                                                                                                                            GQNIHVLSAE---DQCQMETENSVLSHS----AKVSPAEH-----DIQIMSDLHEQSLP-
                                                                                                                                                                                                                                                                                         KKK------RTGSVHHTVAHPAGNLSNKKVTPTAS----TQHDDENDTENGLDTNMH
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5327 AA; !
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chromosome of Drosophila melanogaster.";
the EMBL/GenBank/DDBJ databases.
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                     RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barlow R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Berson K.Y., Benos P. V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bortova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Harris N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Lasko P., L.
Liu X., Mattei B., Mc.
Liu X., Mattei B., Mc.
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Pterygota; I
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01-JUN-2001
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musc
a; Drosophilidae; Drosophila.
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zhence 287:2185-2195(2000).
DR EMBL; AE003750; AAF56376.1; -
DR EMBL; AE003750; AAF56376.1; -
DR EMBL; PE000093; vwr. 1
DR Pfam; PF0001093; vwr. 1
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SMART; SM00214; VWC; 4.
PROSITE; PS01208; VWFC; 1.
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                                                                                                                                                                                                                                                                                                                         EGEVAEKPEDKQPSSTAQAPVETIPEISTELPAQDGDKPTSEAPVDSDEDTSAPSDEKIP
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                                                                                                                                                                                                                                                                                                                                                                                                                         QCNLTKDPNPMSGKERDQVAEQCNLTKDPKPVSGQKCEQICNEPCEEVVLKRSSKSKRKT 338
                                                                                                                                                ----DENDTENGLDINMHKTDVCQHVSEISTQRCSSKGKTAG-LSKGKTHSAASTKYGG
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KKKKKQKLEVTREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDC 655
                                                                                                                   EKEPVDEQEVESGTKATPAESD-GQPIDEIAP--
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                                                      ----EESTTVASA-ASPAVHDDEIKDVTTTQPVADEKEVAAP
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Pred. No. 0.
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RX MEDLINE-20196005, PubMed=JU/J1131,
RA Adams M.D. Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D. Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Burndon R.C., Rogers Y.-H.C., Blazej R.G., Champe N., Pfeiffer B.D.,
RA Burndon R.C., Rogers Y.-H.C., Blazej R.G., Champe N., Pfeiffer B.D.,
RA Burlow R.M., Baster E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Burlow R.M., Baster E.G., Helt G., Nelson C.R., Miklos D.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Barvaktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Broktein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Glan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nison K., Nuskern D.R., Pacleb J.M.,
RA Hilliams R., Tector C., Terring R., Pollard J., Puri V., Reese M.G.,
RA Hilliams R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yirisha R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Rah Glodek R., Gong F.N., Zhon M., Shang G., Zhao Q., Zheng L.,
RA Hilliams R., F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Hilliams R., Tector C., Turner R., Venter J.C.;
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
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Q9W3Z0;
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Q1-MAY-2000
Q1-JUN-2000
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
EMBL; AE003438; AAF46171.1; -
F1yBase; FBgn0029975; CG3950.
SEQUENCE 2951 AA; 332269 MW; 85CCCOABBDAC8A2B
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                    885
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HNSQYAHNQYKGSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPHRPHRPKGV----LGS | | : | | | : : : | | : : : :
                                                  TSTTRGA-----PSKPAQGPIWADRSKVLKGHATVPQTNGSTPRKGSTSSTTSSS--
                                                                                                                                              DLTSTHVMGSSSNYASRQPVIAPLDRYAERAVNQVHARNFP-----STIATMEASK
                                                                                                                                                                                               PGKSSPLPKIRRDQSPAGAA------EVKTKEVRTTTSRRQQQQRVEQV
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                                                                                                                                                                                                                                                                     IEEIFDLQRLEKLLETVASYEMRRRIRAQMRLIR-----KNMINAGTTTTITTTTTSTT
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                                                                                                                        DSTTPIAPGKTSPHG--KPPVKPRERSASPAQKR---RISPPGKQSPGDRSTTTTKVTT
                                                                                     LCDRRNAGQVVLYPKESMPA------THLLR--MMDPSTLASFPNYGTSSRNQMESQL
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Search completed: September 16, 2002, 22:34:15 Job time: 654 sec

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Human polypeptide	AAM39097	22	2663	ω	184.5	5
Drosophila melanog	ABB67502	22	3257	3. 4.	187	44
BRCA1 mutant from	AAR81505	17	1863	3.4	187	43
	ABB59948	22	1489	3.4	187	42
	ABB63410	22	1420	3. 4	187	41
Drosophila melanog	ABB66878	22	2586	3. 4	187.5	ô
~	AAM40002	22	2505	3.4		39
	ABB58514	22	2897		188.5	38
Novel human diagno	ABG06505	22	2633	٠	191.5	37
Murine Natural Kil	AAR13320	12	982		191.5	36
Drosophila melanog	ABB62899	22	3201		192	S
Staphylococcus aur	AAU37018	22	3158	٠	192.5	34
Staphylococcus aur	AAU34207	22	2025	٠	192.5	$\omega$
Drosophila melanog	ABB65391	22	1803	٠	193.5	32
Human carbastatin	AAR05701	1	673		194.5	31
v	ABB68370	22	1730		195	30
Novel human diagno	ABG16636	2 <u>2</u> ,	2519		196.5	29
	AAM80269	22	2515	3.6	196.5	28
protein S	AAM80268	22	2515	•	196.5	27
Human secreted pro	ABB12281	22	2515		196.5	26
	AAR85596	17	694		197	25
Human Protease and	AAY70008	21	754	•	197.5	24
	AAY85577	21	1552		198	23
	ABB61173	22	1690	٠	198.5	22
Drosophila melanog	ABB61144	22	1690		198.5	21
Drosophila melanog	ABB60327	22	3111	٠	200	20
Staphylococcus aur	AAU37120	22	2344		201	19
Drosophila melanog	ABB71460	22	1784		201.5	18
Plasmodium falcipa	AAB18278	21	665		201.5	17
OJ.		10	647		201.5	16
		22	2951		204	15
	ABB68397	22	2768	٠	204	14
ovel human	37	22	2070		206.5	Ω
C. elegans UNC-53	AAW20057	18	1583	٠	208	12

## ALIGNMENTS

AAY84833 RESULT

AAY84833 standard; Protein; 1096 AA

AAY84833;

An isolated nucleic acid molecule comprising embryonic flower genes is useful for modulating reproductive development in plants 09-OCT-1998; WO200022132-A2. Embryonic flower gene-1; EMF-1; reproductive development; flowering; early flowering; uniform flowering. 08-AUG-2000 WPI; 2000-317987/27. N-PSDB; AAA14873. Sung ZR, Aubert D, (REGC ) UNIV CALIFORNIA. 08-OCT-1999; Arabidopsis thaliana. Amino acid sequence of the EMF-1 gene 20-APR-2000. (first entry) 98US-0169696. 99WO-US23543. Chen L;

Claim 7; Page 34-38; 38pp; English.

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MEEMVTIAASSPLFSHHDDQYIAEAPTEHWGRKDAKKLTWEQFKATTRNSPAATCGA---
                                  nntsrppkpcssnarree---hfpmgrqqnshdffpisqpyvpspfgifpptqenr---
                                                                    TNSQQ--KSLASQSTQKELQGHLALTTQESPH-----
                                                                                                      DDIPMDIVELLAKNQHERQLM-TETDCSDINRIQSKTTADDDCVIVAAKDGSDYASSVFD
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                                                                                                                                                                                                           HSAKVSPAEHDIQIMSDL--
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, diagnostics, forensics, gene mapping, identification cresponsible for genetic disorders or other traits and
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Note: The sequence data for this patent did not appear in the printed appear in the printed appear in the printed and the patent for this patent did not appear in the printed as the patent actions of the patent did not appear in the printed as the patent actions of the patent did not appear in the printed as pecification, but was obtained in electronic format directly from WIPO as the patent actions of the patent did not appear in the printed as pecification, but was obtained in electronic format directly from WIPO as the patent actions are patent did not appear in the printed as pecification, but was obtained in electronic format directly from WIPO as the patent actions are patent did not appear in the printed as pecification.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
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food supplement; medical imaging; diagnostic; genetic disorder.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fire.wipo.int/pub/published_pct_sequences.
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene
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Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                            measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exort nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting,
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                                                                                                                                                                                                                                                                                                                                                                                                                      tttsshl 1233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HHDDQYIAEAPTEHWGRKDAKKLTWEQFKATTRN--SPAATCGA--QFRP----GIQAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKNOHEROLMTETDCSDINRIQSKTTADDDCVIVAAKDGSDYASSVFDIN
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                               2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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                                                                                                                                  2001WO-US00666
                                                                                                          2000US-0180312
                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                            hypertension;
                                                                                                                                                                                                                                                           heart; microarray; vascular system;
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          INC
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                                                                                                                                                                                                                                               cardiac
                                                                                                                                                                                                                                               arrhythmia;
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measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                             Penn
                                                                                                                                                                                                                                               Claim 15;
Sequence
                                                                                                                                                                                                              The present
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 1325 AA;
                                                                                                                                                                                                                invention relates to
                                                                                                                                                                                                                                                                                               nucleic acid
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                                                                                                                                                                                                                  nucleic
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δÃ Qy Ωy δÃ B Qy В δÃ 맑 Qy В ρy D Ş 멍 Qy Вþ 밁 В Query Match Best Local Sin Matches 153; Matches 1060 633 587 536 625 576 944 886 480 841 425 786 381 321 692 287 233 113 DKLKTSDNGTAPRTLPAKQNGTSDGCSITFVRSTFVPASVGSQKVSPSTQSSQGKNADRS 172 751 ttp-spaeptenr----ertanenttpsp----agptenremtan---ekttlfpaep TLPKSVQEGNDSKCNAPSGKNGAAEANTDSPMKDLQGPAQNYDVAANVSEDNTSVDVGAL drtplanekttpslaeptengg-----rtpfanekttsssaepteheertplanen PEVPQITWHIEVNGADQPPS----TPKLSEVVLKRNEDENGKTEETLVAEQCNLTKDP-dttpssaeptengertplanentttsptestehgertanekttpspaeptehgertpsan GKTHSAASTKYGG---VTPTAS -- TQHDDENDTENGLDTNMHKTDVCQHVSEISTQRC-----SSKGKTAGLSK GEDGLKSSKNKTKRKYSDVVDDGSSLMNWLNGKKKRTGSVHHTVAHPAGN-----LSNKK 479 nttsspaeptenrertanekttqfpaeptenrestanekttpfpae----ptenrewta EPCEEVVLKRSSKSKRKTDKKLMKKQQHSKKRTAQADVSDAKLCRRKPKKVRLLSEIINA 380 eptenrertanekttpfpaeptenrertane-nttpspaqptengdrtplanekttpsla NPMSGKE----tenrertanekttsspaeptengqrtpfanekttsspaeptehgertplane-nttlspa 691 AKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSDYASSVFDTN--ektipspakptehe-emtpsanenttpspvkptehgekttlanekitlspegp-------VSPAEHDIQIMSDLHEQSLPKKKKK---ttpssaeptehgertplanei-ttpsraeptehgerianekatpspakptehgett-vne nenttlspaepteh----NQVEDSRSDEVHRENA - - - epteng--krtpfanekttsssaeptehaer----Similarity Conservative 19.4%; eemtplan----ekttls----paeptengertpftnek 125; ---ADPCEDDRS----TIPVPMEVSMDIPVSNH--TV Score 220; DB 22; Pred. No. 9.7e-08; 5; Mismatches 311; ----ESTRNGQNIHVLSAEDQCQMETENSVLSHSAK RDQVAEQCNLTKDP-----KPVSGQKCEQICN -QKLEVTREKQTMIDDIPMDIVELL Length 1325; -----tplane Indels 198; Gaps 1003 424 785 750 320 943 885 286 674 38;

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                                                                                                                                                        Matches 153;
                                                                                                                                                                                                                       Query Match
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
21 - SEP - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by the present encoded by the present encoded by the present encoded by the present encoded by the p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single exon nucleic acid brains -
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                                                                                                                                                                                                                                                                                                                                   Sequence
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           536
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                                                                      113 DKLKTSDNGTAPRTLPAKQNGTSDGCSITFVRSTFVPASVGSQKVSPSTQSSQGKNADRS 172
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drtplanekttpslaeptengg-----
                                                                                                                                                                                      Similarity
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                                                                                                                                                    Conservative 125;
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                                                                                                                                                 Score 220; DB 22;
Pred. No. 9.7e-08;
5; Mismatches 311
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                                                                                                                                                    311;
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ARMSOLUT
AAMSOLUT
AAM

Human bone marrow expressed probe

06-NOV-2001 AAM68085; AAM68085

(first entry)

Homo

sapiens

WO200157276-A2

microarray; Human; bone

cancer;

leukaemia; lymphoma; myeloma

exon; gene expression

probe

encoded protein

SEQ ID analysis; Š

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standard;

Protein; 1325

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tttsshl 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                            dttpssaeptengertplanentttsptestehgertanekttpspaeptehgertpsan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEDGLKSSKNKTKRKYSDVVDDGSSLMNWLNGKKKRTGSVHHTVAHPAGN-----LSNKK
                                         DLTSTHV 790
                                                                                 kgkntpvpekptenlgn---ttlttetikapvkstenpektaavtktikpsvkvtgdksl 1226
                                                                                                                                                                      khakrttlahekmtq-----vtekstehpekttsttektt--rtpekptlysektict 1169
                                                                                                                                                                                                                -- SQQKSLASQSTQKELQGHLALTTQESPHPQNFQSTQEQQTHLRMEEMVTIAASSPLFS
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                                                                                                                          HHDDQYIAEAPTEHWGRKDAKKLTWEQFKATTRN--SPAATCGA--QFRP----GIQAV
                                                                                                                                                                                                                                                                                                          AKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSDYASSVFDTN------
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
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                                            dttpssaeptengertplanentttsptestehgertanekttpspaeptehgertpsan
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                                                                                                                                                                                                                                                                                                                                                     eptenrertanekttpfpaeptenrertane-nttpspaqptengdrtplanekttpsla
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--VSPAEHDIQIMSDLHEQSLPKKKKK----QKLEVTREKQTMIDDIPMDIVELL
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2000US-0207456.
2000US-0508408.
2000US-0632366.
2000US-0234369.
2000US-0236359.
2000US-0236359.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 220; DB 22;
Pred. No. 9.7e-08;
%5; Mismatches 311;
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                                                                         ESTRNGQNIHVLSAEDQCQMETENSVLSHSAK 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1325;
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26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                      Probe; human; breast disease; breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM03645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM03645 standard;
                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #2327 encoded by probe
                                                                                                                                                                Novel single exon nucleic acid in a human breast -
                                                                                                                                                                                              WPI; 2001-476286/51
                                                                                                                                                                                                                Penn
                                                                                                                                                                                                                                                               21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                  29-JAN-2001; 2001WO-US00661
                                                                                                                                                                                                                                                                                                                                                                      WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    784
                                                                                                                                              Claim 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --SQQKSLASQSTQKELQGHLALTTQESPHPQNFQSTQEQQTHLRMEEMVTIAASSPLFS
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                                                                                                                                                                                                                SG,
                                                                                                                                                                                                                                   MOLECULAR DYNAMICS INC
                                                                                                                                             SEQ ID No 12385; 322pp; English.
                                                                                                                                                                                                                Hanzel
                                                                                                                                                                                                                                                     2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                DK,
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                                                                                                                                                                                                                                                                                                                                                                                                            proliferative
                                                                                                                                                                                                                  Chen
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                                                                                                                                                                           probe used to
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                                                                                                                                                                                                                  Rank
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                                                                                                                                                                                                                                                                                                                                                                                                             cancer; develo
breast disease;
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                                                                                                                                                                             measuring
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The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences.

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 apoptosis associated protein YMR230W.
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The present invention provides the protein and coding sequences of a number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identify treatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaemia and neurodegeneration. The present sequence is one of the S. cerevisiae
                                                                                                                                                                                                                                                                                                             Yeast and fungal nucleic acids encoding proteins involved in a pathway leading to programmed cell death, useful for treating proliferative disorders, yeast and fungal infections, or for preventing apoptosis in certain diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeast; fungus; apoptosis; infection; proliferative disease; vaccine; autoimmune disease; ischaemia; neurodegeneration.
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Nelissen BJM,
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Query Match Best Local S Matches 204 527 192 387 140 327 115 267 213 155 QKVSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAEANTDSPM--KDLQGPAQ 59 Match 3.9%; S. Local Similarity 18.7%; P. Local Similarity 18.7%; P. Local Similarity 156; σ GLSKGKTHSAASTKYGGESTRNGQNIHVLSAEDQCQMETENSVLSHSAKVSPAEHDIQIM -lsnpssslrnkkssllvasn----higsvsst-nnnsnnalinhnplssh-----NYDVAANVSE-----DNTSVDVGALPEVPQITWHIEVNGADQPPSTPKLSEVVLKRNED rkltvetetveapvannlll-----snnsnvvapnpsipsastst-splhreivddsva 58 **pnhsnaddnennnkmkknkninsgknernddtskicttstktapstaplgstdntqalta** PTASTQHDDENDTENGLDTNMH-----KTDVCQHVSEISTQRCSS --lsqqnkpkilerptmhvtnsreillgenllddtkaknapanst-thdngpvandglri GLKSSKNKTK---RKYSDVVDDGSSLM--NWLNGKKKRTGSVHHTVAHPAGNLSNKKV-T rsanihgpsstsaskafrkasafsnntapstsnnigsntppapl.----lplps----RSDEVHRENAADPCEDDR-----VLKRSSKSKRKTDKKLMKKQQHSKKRTAQADVSDAKLCRRKPKKVRLLSEIINANQVEDS 386 ENGKTEETLVAEQCNLTKDPNPMSGKERDQVAEQCNLTKDPKPVSGQKCEQICNEPCEEV 326 tanttsnvvqhnlptidnnlmdsdatsh-nqdhwhsdinragtsmst---sdiptdlhle 114 Score 217; DB 22; Pred. No. 1.4e-07; 6; Mismatches 416 -pafasdvelskkkpavisnnmptsnialyqta ---STIPVPMEVSMDIPVSNHTVGED Indels ------KGKTA 526 314; -Gaps 586 297 481 427 191 212 357 240 139 46;

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STRINGHAM E.
VANDEKERCKHOVE J.
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UNC-53 protein variants 8A and 7A of Caenorhabditis elegans are new. The UNC-53 proteins and nucleic acids are useful as medicaments to promote neuronal regeneration, revascularisation or wound healing, or for treatment of chronic neurodegenerative diseases (e.g. Alzheimer's or Huntingdon's disease) or acute traumatic injuries. Transgenic cells and organisms transfected with UNC-53 CDNA can be used to determine whether a substance is an inhibitor or enhancer of the regulation of cell shape or motility or the direction of cell migration by screening for a phenotypic change in the cell. Inhibitors can be used to alleviate the spread of disease inducing cells or metastasis. Probes derived from the CDNA sequences can be used to identify homologues of the C. elegans unc-53 gene. The UNC-53 protein can be used to identify proteins which
                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans UNC-53 protein 8A and 7A variants - promote neuronal regeneration, revascularisation or wound \dot{r}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-034369/03.
N-PSDB; AAT71315.
Sequence
                                                                   are active in the signal transduction pathway that can be used
                                                                                                                                                                                                                                                                                                                                                                                             Claim 22; Page 111-116;
                                                above
  1583 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                English.
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Query Match Best Local S Matches 231 342 440 383 291 274 239 224 184 167 128 68 83 lgldcskltktdidsgnlgavlqllfllstykg-14 VGTNCM-----LARGGTGAVAPVLELTATPRODAAAEAGVDEPAQHQCEHFSIRGYVAL Local Similarity 19.5 les 231; Conservative IHVLSAEDQCQMETENSVLSH-SAKVSP----AEHDIQIMSDLHEQSLPKKKKKQKLEV LMKKQQHSKKRTAQADVSDAKLCRRKPKK----VRLLSEIINANQVEDSRSDEVHRENAA LQKKDPKFCSLSRIFHDQKKCDEHKASSSPFSVAKFRRWDCSKCLDKLKTSDNGTAPRTL idt----tdvpplpplksvvplkmtsirqpptydvllkqgkitspvks-fgyeqs----pppavpprdt-----qptigvvspimah-----kkltndpvisekpepeklqsms sstsdekspssddltlnasivtairqpiaatpvspniinkpveekptlavkgvkstakkd DPCEDDRSTIPVPMEVSMDI------PVSNHTVGED-----GLKSSKNKTKRK iisqq-----dskrcsksseeesgyagfnstsptssstegsls--mhstssk ----sklaapkavstpklasvktigakqepdnsggggggmlklklfssknpssssnspqp TWHIEVNGADQPPSTPKLSEVV----LKRNEDENGKTEETLVAEQCNLTKDP-----NPMS stistsakslessstyssisnlnrptsqlqkpsrpqtqlvrva---tttkigs----tsrlqtpqsriskidsskigikpktsglkppsssttssnntnsfr---pssrssgnnnvg PAK-QNGTSDGCSITFVRSTFVPASVGSQKVSPSTQSSQGKNADRSTLPKSVQEGND---LDTNMHKTDV--CQHVSEISTQRCSSKGKTAG----LSKGKTHSAASTKYGGESTRNGQN YSDVVDDGSSLMNWLNGKKKRTGSVHHTVAHPAGNLSNKKVT--PTASTQHDDENDTENG trkaaavpqqqtlskiaapvksglk-----pptsklgsatsmsklctpkvsyrktdap -----klrqlkkdqkkleqlptsimppavsklpsprvatsatasatnpnsnfpqms 166 -SKCNAPSGKNGAAEANTDSPMKDLQGPAQNYDVAANVSEDNTSVDVGALPEVPQI -sasedsivahasaqvtpptktsgnhsl----3.8%; 18; Score 208; DB 18; 18; Pred. No. 1.1e-06; 174; Mismatches 427 Length 1583; errmgknktsessgy Indels 350; Gaps 439 397 341 67 487 427 238 582 532 497 382 329 290 273 223 183 57;

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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                       31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG03703 standard; Protein; 2070
                                                                         WPI; 2001-639362/73.
N-PSDB; AAS67890.
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                                                                                                                                                                                                                                                                      WO200175067-A2
                                                                                                                                                                                                                                                                                                                                           Human; chromosome
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                                                                                                                  Drmanac
                                                                                                                                            (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kllsqcrtsqrg-----aaatstfgqhslrspgyssysp--hls-vsadkdtmsm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AD---DDCVIVAAKDGSDYASSY-FDTNSQQK----SLASQSTQKELQGHLALTTQESPH
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                                                                                                                  RT,
                                                                                                                                                                       2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                  Liu C,
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medical imaging; diagnostic; genetic disorder
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Claim 20; SEQ ID No 34062; 103pp; English.

The invention relates to isolated polynucleotide (I) and colypeptide (II) sequences. (I) is useful as hybridisation probes, complymerase chain reaction (PCR) primers, oligomers, and for chromosome cand gene mapping, and in recombinant production of (II). The colynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (I), (II) is useful for generating antibodies against it, detecting or comparing the polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating imaging of sites expressing (II). (I) and (II) are useful for treating comparing of the polypeptide and polynucleotide sequences have applications in constitus, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cand sequences. ABG00010-ABG30377 represent novel human continuations of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO can be produced to the print of the polypeptide and products of the invention. ftp.wipo.int/pub/published_pct_sequences

Sequence 2070 AA;

Query Match

Local Similarity

DB 22;

Length 2070

맑 QΥ Вb Qy Дb Qy 밁 QΥ δÃ 밁 δõ B Ωy 밁 δÃ 밁 B Qy Дb Matches 1184 1241 1024 1075 364 -- CRRKPKKVRLLSEIINANQVEDSRSDEVHRENAADPCEDDRSTIPVPMEVSMDIPVSN 421 974 -dfs-----senpkivdssvnlhpkqelllmnnddrdppqhhsclpdqevingsli 1023 920 veliaepcrveqdssdtmqttgllkgqglttllsdlakkknpqksslsdq-mdhp-----92 57 1 MEIVA----VDQEGARVVGTNCMLARGGTGAVAPVLELTATPRQDAAAEAGVDEPAQHQC srcispsxstistxssssssssssssnsnnnkqgsxergityikcsimylmqralstlsp 1452 gtgqae----atpnefnsqgsieatmerplekpscslgiktsnaslqdstsqppsitsl 1183 FVPASVGSQKVSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAEANTDSPMKD 206 pknsxipmtstipnsqiqepllkpshesrk-----dsakravqddlllssakrq 1289 PKPVSGOKCEQICNEPCEEVVLKRSSKSKRKTDKKLMKKQQHSKKRTAQAD--VSDAKL- 363 svnnlihqssishplascaglsptseqttvpatvnltvssssygsqppgtisdvlni---SEVVLKRNED-----ENGKTEETLVAEQCNLTKDPNPMSGKERDQVAEQCNLTKD 306 LQGPAQNYDVAANVSEDNTSVDVGALP----EVPQITWHIEVNGA------DQPPSTPKL 256 xyssscsksyfxp-----gepxegeswppgxykgssskpseasllegdppfksqipkes 1128 ngrqadspmstssgssrsfsvasmlpettred-----KASSSPFSVA--KFRRWDCSKCLDKLKTSDNGTAPRTLPAKQNGTSDGC-SITFVRST 146 EHFSIRGYVALLQKKDPKFCSLSRIFH-----DQKKCDEH------231; QRCSSKGKTAGLSKGKTHSAAS---pahg-dgltrlfppsnnfvtpalrqtevqcgsqps---vaeqqqtqasqhlqasaaacss HTVGEDGL-----KSSKNKTKRKYSDVVDDGSSLMNWLNGKKKRTGSVHHTVAHPAGNLS 476 khcqpaplrlesmslm---srtpdtisdqtqmmvsqippnssnsv---Conservative 3.7%; Score 206.5; DB 22; 19.1%; Pred. No. 2.3e-06; tive 188; Mismatches 509; ----TKYGGESTRN------vtsnattntcdsctfvetn 1074 Indels 279; -----vpvsn 1336 -VSEIST --GQNI 552 Gaps 56 1240 91 973 1392 53;

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                                                                                                                                                                                                                     Drosophila;
                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide
                                                                                                                                                                                                                                                                                               ABB68397;
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WPI; 2001-656860/75
                                                                       23-MAR-2000;
11-JUL-2000;
                                                                                                          23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                      26-MAR-2002
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                       Venter JC,
                                            (PEKE ) PE
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                       Adams M,
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                                                                      2000US-191637P
2000US-0614150
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                                                                         LLQKEIANWSENCGTQ---SGYKLG---VSTGITSHQMNRKEHFEALNSGMFSAKWNALQ
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1: /cgn2_6/ptodata/2,

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US-08-8603-753D-2
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US-08-825-866-22
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US-08-825-866-24
US-08-483-553-2
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                       999 KRNQTVDTTNIT-----TPNDI--QADAPSAQSNNEEIARVETPVPPP-----A 1040
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Sequence 1, Appli	Sequence 2, Appli	Sequence 50, Appl	Sequence 8, Appli	Sequence 189, App	Sequence 5, Appl1	Sequence 5, Appli	Sequence 2, Appli	Sequence 16, Appl	Sequence 16, Appl	Sequence 6, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 4, Appli

ALIGNMENTS

Title:

Run on:

## TELEFAX: (415) 398-32 TELEX: 910 277299 INFORMATION FOR SEQ ID NO: GENERAL INFORMATION: CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,801 REFERENCE/DOCKET NUMBER: A-59941/RFT/RMS TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989 TELEPAX: (415) 398-3249 ZIP: 94111-4187 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: SEQUENCE CHARACTERISTICS: LENGTH: 1848 amino aci APPLICANT: St. Geme III, Joseph APPLICANT: Falkow, Stanley TITLE OF INVENTION: Haemophilus TITLE OF INVENTION: Protein NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California APPLICATION NUMBER: US/0 FILING DATE: 25-AUG-1994 CLASSIFICATION: 435 ADDRESSEE: Flehr, Hohbach, Test, Albritton 6, Application US/08296791 o. 6245337 amino acid GY: unknown 1848 amino acids United States Haemophilus Adherence and Penetration US/08/296,791 6. δ.

3.7%; 18.5%;

Score 202.5; DB 4; Pred. No. 8.7e-07; 1; Mismatches 403;

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RESULT 2
PCT-US95-10661A-6
                                                                                                                                                                                                                   Sequence 6, Application PC/TUS9510661A GENERAL INFORMATION:
                                                                                                                NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESQLHNSQYAHNQYKGSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPLRPHPRVGVLGS 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVISNAMAKAQFVALNVGKAV-----SQHISQL-----EMNNEGQYNVWISNTSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAPQVTSKEPPKQA------EPAPEEVPTDTNAEEAQALQQTQPTTV-AAAET 1250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKPVSGQKCE----QICNEPCEEVVLKRSSKSKRKT----DKKLMKKQQHSKKRTAQAD 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPSET---TEKVAENPPQEN----ETVAKNEQEAT-EPTPQNGEVAKEDQPTVEANTQTN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPPSTPKLSEVVLKRNEDENGKTEETLVAEQCNLTKDPNPMSGK--ERDQVAEQCNLTKD 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSGKNGAAEANTDSPMKDLQGPAQNYDVAANVSEDNTSVDVGALPEVPQITWHIEVNGAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNSPAATCGAQFRPGIQAVDLTSTHVMGSSSNYASRQPVIAPLDRYAERAVNQVHARNFP 824
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                  California
                                                             E: Flehr, Hohbach, Test, Albritton
4 Embarcadero Center, Suite 3400
                                                                                                                                                              Washington University, et al. VENTION: Haemophilus Adherence and
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                                                                                     & Herbert
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Query Match
Best Local Similarity
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                                                                                                                                                       1371
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LENGTH: 1848 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/106
FILING DATE: 16-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                       473
                                                                                                                                                                                                                                                                                                                                                                            418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 25-AU CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: FP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COERNATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Trecartin, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
  DDCVIVAAKDGSDYASSVFDTNSQQKSLASQSTQKELQGHLALTTQE-----
                                                                PAPENSINTGSATTMTETAEKSDKPQ--METVTENDRQPEANTVADNSVANNSESS----
                                                                                                                                                                                                                                                                                GNLSNKKVTPTASTQHDDENDTENGLDTNMHKTDVCQHVSEISTQRCSSKGKTAGLSKGK 532
                                                                                                                                                                                                                                                                                                                                                                         PVSNHTVGEDGLKSSKNKTKRKYSDVVDDGSSLM-----NWLNGKKKRTGSVHHTVAHPA 472
                                                                                                                                                                                                                                                                                                                                                                                                                     KAPQVTSKEPPKQA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EATQSEGKTEETQTAETKSEPTESVTVSENQPEKTVSQSTEDKVVVEKEEKAKVETEETQ 1204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATESAIASEQPETRPAETAQPAMEETNTANSTETAPKSDTATQTENP-----NSES 1092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRNQTVDTTNIT-----TPNDI--QADAPSAQSNNEEIARVETPVPPP------A 1040
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                                                                                                       SLPKKKKKQKLEVTREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTAD
                                                                                                                                                                                           THSAASTKYGGESTRNGQNIHVLSAEDQCQMETENSVLSHSAKVSPAEHDIQIMSDLHEQ 592
                                                                                                                                                                                                                                         PKQEQPAAKPQAQTKPQAEPARENVLTTKNVGEPQPQAQPQTQSTAVPTTGETAANSKPA 1370
                                                                                                                                                                                                                                                                                                                              TSPNSKPAEETQQPSEKTNAEPVTPVVSENTATQPTETEETAKVEKEKTQEVPQVASQES 1310
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415) 398-3249
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Patent No. 5622829
                                                                                                    TELEFAX: (415) 494-877
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8770
TELEFAX: (415) 494-8771
TELEFAX: (415) 494-8771
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APPLICANT: KING,
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
STATE: California
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: GENETIC MARKERS FOR BREAST TITLE OF INVENTION: CANCER
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                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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TOPOLOGY: 1
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                               STRANDEDNESS:
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                                                                   ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLQKEIANWSENCGTQSGYKLGVSTGITSHQMNRKEH------FEALNSG
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                                                                                                                                                                                                                                                                                                                                                                                                                            94111-4187
                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT 4 Embarcadero Center, Suite 3400
                                                               900 amino acids
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FRIEDMAN, Lori
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LYNCH, Eric
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protein
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US-08-425-061-20

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Best Local Similarity
Matches 200; Conserv 515 315 216 147 844 634 583 532 482 471 424 421 368 371 324 SKETCND-----RRTPSTEKKVDLNADPLCERKEWNKQKLP-----CSENPRDT 367 270 157 732 694 276 VAEQCN-------LTKDPNPMSGKERDQVAEQCNLTKDPKPVSGQK----204 104 RRWDCSKCLD-----87 LKIICAFQLDTGLEYANSYNFAKKENNSPEHLKDEVSIIQSMGYRNRAKRLLQSEPENPS 31 IKEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLCKNDITKRSLQE----STRFSQLVEEL 48 VDEPAQHQCEHFSIRGYVALL -- QKKDPKFCSLSRIFHDQKKCDEHKASSSPFS -- VAKF 103 VVLYPKESMPATHLLRMMDPSTLASFPNYGTSSRNQMESQLHNSQYAHNQYKGSTSTSYG 903 ----VRLLSEIINANQVEDSRSDEVHRENAADPCEDDRSTIPVPMEVSMDI-----PVS QLMTE---TDCSDINRIQSK-----TTADDDCVIVAAKDGSDYASSVFDTNSQQKSLAS ---STORCSSKGKTAGLSKGKTHSAASTKYGGESTRNGONIHVLSAEDOCOMETENSVLS GSSEKIDLLASDPHEALICKSERVHSKSVE--SNIEDKIFGKTYRKKASLPNLSHVTENL 481 NHTVGEDGLKSSKN-----KTKRKYSDVVDDGSSLMNWLNGKKKRTGSVHHTVAH-----CEQICNEPCEEVVLKRSSKSKRKTD---KKLMKKQQHSKKRTAQADVSDAKLCRRKPKK-HVEPCGTNTHASSLQHENSSLLLTKD-----RMNVEKAEFCNKSKQPGLARSQHNRWAG VAANVSEDNTSVDVGALPEVPQITWHIEVNGADQPPSTPKLSEVVLKRNEDENGKTEETL 275 LLQIT-----PQGTRDEISLDSAKKAACEFSETDVTNTEHHQPSNN--VSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAE-ANTDSPMKDLQGPAQNYD 215 -----KLKTSDNGTAPRTLPAKQNGT------SDGCSITFVRSTFVPASVGSQK 156 SHHDDQYIAEAPTEHWGRKDAKKLTWEQFKATTRN-----SDTFPELK----LTNA----PGSFTKCSNTSELKEFVNPSLPREEKEEKLETVKVSNN--QSTQKELQGHLALTTQESPHPQNF---QSTQEQQTHL-----RMEEMVTIAASSPLF 731 PNCTELQIDSCSSSEEIKKKKYNQMPVRHSRNLQLMEGKEPATGAKKSNKPNEQTSKRHD 693 KAEPISSSISNMELELNIHNSKAPKKNRLRRKSSTRH-----IHALELVVSRNLSP HSAKVSPAEHDIQIMSDLHEQSLPKKKKKQKLEVTREKQTMIDDIPMDIVELLAKNQHER 631 INQGTNQTEQNGQVMNI----TNSGHENKTKGDSIQNEKNPNPIES----LEKESAFKT IIGAFVTEPQIIQERPLTNKLKRKRRPTSGLHPED-----FIKKADLAVQKTPEM -----PAGNLSNKKVTPTASTQHDDENDTENGLDTNMHKTDVC-QHVSEI 514 EDVPWITLNSSIQKVNE-WFSRSDEL---LGSDDSHDGESESNAKVADVLDVLNEVDEYS -----EKRAAERHP--LQETSLSVQLSNLGTV-RTLRTKQRIQPQKTSVYIELGSDSSEDTVNKATY--CSVGDQE 203 SLLEVSTLGK----AKTEP----DLTSTHYMGSSSNYASRQPVIAPLDRYAERAVNQVHARNFPSTIATMEASKLCDRRNAGQ 843 ----AEDP-----KDL-MLSGERVLQTERSVESSSISLVPGTDYGTQ-----ESI 3.3%; Score 182; DB 1; Length 900; ilarity 18.4%; Pred. No. 1.2e-05; Conservative 142; Mismatches 363; Indels : ----NKCVSQCAAFENPKGL-IHGCSK--DNRNDTE 827 -SPAATCGAQFRPGIQAV 783 Indels 382; ----EKYQGSSVSNL Gaps 682 146 571 531 423 370 323 86 470 420 269 743 314 244 49;

Qy 104 RRWDCSKCLD	Qy 48 VDEPAQHQC :   :   :   Db 31 IKEPVSTKC	Query Match Best Local Similarity Matches 200; Conser	; TOPOLOGY: 11; MOLECULE TYPE: US-08-825-886-20	SEQUENCE CHARACTERISTICS; SEQUENCE CHARACTERISTICS; LENGTH: 900 amino acid TYPE: amino acid	; TELEPHONE: ; TELEFAX: (4 ; TELEX: 910	; ATTORNEY/AGENT INFORMA ; NAME: OSMAN, RICHAT; REGISTRATION NUMBER: REFERENCE/DOCKET NUM ;		CURRENT APPLICATION  APPLICATION  FILING DATE:	COMPUTER REALIBETE FORM:  MEDIUM TYPE: Floppy COMPUTER: IBM PC com OPERATING SYSTEM: PC COFFERED BY: Datastin B	; CITY: San Franc ; STATE: Californ ; COUNTRY: USA ; ZIP: 94111-4187	ONDENC ONDENC SSEE:	APPLICANT: LEE, MI FITLE OF INVENTION: TITLE OF INVENTION:	APPLICANT: FK.  APPLICANT: OS:  APPLICANT: ROI  APPLICANT: LYI  APPLICANT: SZZ	; Patent No. 5821328 ; GENERAL INFORMATION: ; APPLICANT: KING,	886-2	Qy 964 STGITSH 97 	871	Db 828 GFKYP
LD	VDEPAQHQCEHFSIRGYVALLQKKDPKFCSLSRIFHDQKKCDEHKASSSPFSVAKF 103	3.3%; Score 182; DB 2; Length 900; arity 18.4%; Pred. No. 1.2e-05; onservative 142; Mismatches 363; Indels 382; Gaps 49;	inear protein	ACTERISTICS:  Damino acids Dacid	94-87 -8771	TORREY/AGENT INFORMATION:  NAME: OSMAN, Richard A REGISTRATION NUMBER: 36,627 REFERENCE/DOCKET NUMBER: A-59563-3/DJB/RAO	ON: TION DATA: NUMBER: 08/425,061	ON DATA: BER: US/08/825,886	disk patible -DOS/MS-DOS	California USA 111-4187	ENCE ADDRESS:  E: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  4 Embarcadero Center, Suite 3400	TION: GENETIC MARKERS FOR BREAST AND OVARIAN TION: CANCER	FRIEDMAN, LOTI OSTERNEYER, Beth ROWELL, Sarah LYNCH, Eric SZARD, Csilla	Mar	100+100 IIG/08805886	970 899		GFKYPLGHEVNHSRETSIEMEE:ELDAQYLQNTFKVSKRQSFA 870
RESUI	Db 43	Qy Db	Qy Db	Qy Db	Qy Db	Qy	Qу	Qy Db	ОУ	Qy Db	Qу	Оy	Qy .	Ф	Qу	Фр	Db	Db
RESULT 5 US-08-603-753D-2	KTKSKSH	904 SNLNGKIPLTFEDLSRHQLHDLHRPLRPHPRVGVLGSLLQKEIANWSENCGTQSGYKLGV 963 871PFSNPGNAEEECATFSAHSGSL 892		784 DLTSTHVMGSSSNYASROPVIAPLDRYAERAVNQVHARNFPSTIATMEASKLCDRRNAGQ 843	732 SHHDDQYIAEAPTEHWGRKDAKKLTWEQFKATTRNSPAATCGAQFRPGIQAV 783	683 OSTQKELQGHLALTTQESPHPQNFQSTQEQQTHLRMEEMVTIAASSPLF 731	632 QLMTETDCSDINRIQSKTTADDDCVIVAAKDGSDYASSVFDTNSQQKSLAS 682	572 HSAKVSPAEHDIQIMSDLHEQSLPKKKKKQKLEVTREKQTMIDDIPMDIVELLAKNQHER 631 583 KAEPISSSISNMELELNIHNSKAPKKNRLRKKSSTRHIHALELVVSRNLSP 633	515STQRCSSKGKTAGLSKGKTHSAASTKYGGESTRNGQNIHVLSAEDOCQMETENSVLS 571	471PAGNLSNKKVTPTASTQHDDENDTENGLDTNMHKTDVC-QHVSEI 514	421 NHTVGEDGLKSSKNKTKRKYSDVVDDGSSLMNWLNGKKKRTGSVHHTVAH 470	371VRILSEIINANQVEDSRSDEVHRENAADPCEDDRSTIPVPMEVSMDIPVS 420 :	315 CEQICNEPCEEVVLKRSSKSKRKTDKKLMKKQQHSKKRTAQADVSDAKLCRRKPKK- 370 ::     : ::       ::: :   :       :::       :::           :::	276 VAEQCN	216 VAANVSEDNTSVDVGALPEVPQITWHIEVNGADQPPSTPKLSEVVLKRNEDENGKTEETL 275	157 VSPSTQSSQGKNADRSTLFRSVQEGNDSKCNAPSGKNGAAE-ANTDSFMKDDQGFMQNID 213 :	LQETSLSVQLSNLGTV-RTLRTKQRIQPQKTSVYIELGSDSSEDTVNKATYCSVGDQE	87 LKIICAFQLDTGLEYANSYNFAKKENNSPEHLKDEVSIIQSMGYRNRAKRLLOSEPENPS 146 114KLKTSDNGTAPRTLPAKQNGTSDGCSITFVRSTFVPASVGSQK 156

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Patent No.
GENERAL II
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FILING DATE: 17 JAN 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
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TITLE OF
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REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WORD PERFECT 6.1 and ASCII CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
NUMBER OF SEQUENCES: 29
                                                                       FEATURE:
                                                                                                                                            CLONE: obtained using POSITION IN GENOME:
                                                                                                                                                                           LIBRARY: CDNA
                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE:
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APPLICANT: THOMPSON, MARILYN E.
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                                                                                                                                                                                                          DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
CELL TYPE: ductal carcinoma in situ, invasive
CELL TYPE: breast cancer and normal breast tissue
CELL LINE: not derived from a cell line
ORGANELLE: no
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: unknown
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NAME/KEY: BRCA1 protein LOCATION: 1 to 1863 IDENTIFICATION METHOD: (IDENTIFICATION METHOD: ()
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                                                                                                         MAP POSITION:
                                                                                                                         CHROMOSOME/SEGMENT:
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                                                                                                                                                                                                                                                                                                                                         ORGANISM:
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                                                                                        unknown
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                                                                                                                                                       cDNA library derived from human
btained using published sequence
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KING, MARY-CLAIRE
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Best Local Similarity
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AUTHORS: Miki, Y., et
 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS: Miki, Y., et. al.
TITLE: A strong candidate gene for the breast and
TITLE: ovarian cancer susceptibility gene BRCAl.
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DIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSDY-----
                               KRHDSDTFP---ELKLTNAPGSFTKCSNTSELKEFVNPSLPREEKEEKLETVKVSNNAED
                                                                                                                           TQRCSSKGKTAGLSKGKTHSAASTKYGGESTRNGQNIHVLSAED-----QCQMETENSV
                                                                                                                                                           AEPISSSISNEL---ELNIMHNSKAPKKNRLRRKSSTRHIHALELVVSRNLSPPNCTELQ
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GENERAL INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/603,753
FILING DATE: 20 FEB 1996
APPLICATION NUMBER: U.S. 08/373,799
ETILING DATE: 17 JAN 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ROBINSON-BENION, CHERYL L.
APPLICANT: THOMPSON, MARILYN E.
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                    MEDIUM TYPE: Diskette, 3.50 inch, COMPUTER: IBM PC/XT/AT compatible OPERATING SYSTEM: Windows 3.1
                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                CLASSIFICATION:
                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 27707
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JENSEN, ROY A.
PAGE, DAVID L.
KING, MARY-CLAIRE
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JETTON, THOMAS L.
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VOLUME: 266
; PAGES: 66-71
; PAGES: 1994
; DATE: 1994
; RELEVANT RESIDUES I
; RELEVANT RESIDUES I
US-09-099-753-2
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: cDNA library
CLONE: obtained using
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
AUTHORS: Miki, Y., et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
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CELL TYPE:
CELL LINE:
                               216 VAANVSEDNTSVDVGALPEVPQ-----ITWHIEVNGADQPPSTPKLSEVVLKRNEDEN 268
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                                                                                                                                                                                                                                                                104 RRWDCSKCLD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (919) 419-0383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION METHOD: antisense inhibition of BRCA1 gene OTHER INFORMATION: BRCA1 protein has a negative OTHER INFORMATION: regulatory effect on growth of human mammary cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
                                                                                                                                                                                                                            87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS: Miki, Y., et. al.
TITLE: A strong candidate gene for the breast and
TITLE: ovarian cancer susceptibility gene BRCAl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE TYPE:
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                                                                                                                                                                                                                                                                                                 31 IKEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLCKNDITKRSLQE----STRFSQLVEEL 86
                                                                                                                                                                                                                                                                                                                                        48 VDEPAQHQCEHFSIRGYVALL--QKKDPKFCSLSRIFHDQKKCDEHKASSSPFS--VAKF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD: observation of mRNA and IDENTIFICATION METHOD: antisense inhibition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: BRCAl protein LOCATION: 1 to 1863
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                                                                                                                                                                                                                        LKIICAFQLDTGLEYANSYNFAKKENNSPEHLKDEVSIIQSMGYRNRAKRLLQSEPENPS 146
                                                                                                          VSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAE-ANTDSPMKDLQGPAQNYD
                                                                                                                                               LQETSLSVQLSNLGTV-RTLRTKQRIQPQKTSVYIELGSDSSEDTVNKATY--CSVGDQE
                                                                                                                                                                                   -----KLKTSDNGTAPRTLPAKQNGT------SDGCSITFVRSTFVPASVGSQK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                                          3.3%; Score 180; DB ilarity 17.9%; Pred. No. 5.2e Conservative 174; Mismatches
DINTTEKRAAERHPEKYQGSSVSNIHVEPCGTNTHASSIQHENSSILLIKDRM 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science
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breast cancer and normal breast
not derived from a cell line
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ
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5.2e-05;
hes 387;
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524 AVOKTPEMINOGTNOTEONGOVNNITNSGHENKTKGDSIONEKNPNPIESLEKESAFKTK 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNYASRQ------PVIAPLDRYAE-RAVNQVHARNFPSTIATM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QSPKVTFECEQKEENQGKNESNIKPVQTVNITAGFPVVGQKDKP----VDNAKCSIKGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSHSAKVSPAEHDIQI-------MSDLHE---QSLPKKKKKQKLEVTREKQTMID 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDSCSS-----SEEIKKKKYNQMPVRHSRNLQLMEGKEPATGAKKSNKPNEQTS 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TQRCSSKGKTAGLSKGKTHSAASTKYGGESTRNGQNIHVLSAED-----QCQMETENSV 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEPISSSISNEL---ELNIMHNSKAPKKNRLRRKSSTRHIHALELVVSRNLSPPNCTELQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NVEK----AEFCNKSKQP----GLARSQHNRWAGSKETCN---DRRTPSTEKKVDLNADP
                                                                                                                                                                                                                                           IANWSENCGTQSGYKLGVSTGITSHQMNRKEHFE
                                                                                                                                                                                                                                                                                     SNINEVGSSTNEVGSSIN-EIGSSDENIQAELGRNRGPKLNAMLR-----LG-VLQPE 1092
                                                                                                                                                                                                                                                                                                                                  HN-QYKGSTSTSYGSNLNGKIPLTFE----DLSRHQLHDLHRPLRPHPRVGVLGSLLQKE 945
                                                                                                                                                                                                                                                                                                                                                                              EEHSMSPEREMG-----NENIPST------VSTISRNNIRENVFKEASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RFCLSSQFRGNETGLITPNKHGLLQNPYRIPPLFPIKSFVKTKCKKNLLEENF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMEE-----SELDAQYLQNTFKVSKRQSFAPFSNPGNAEEECATFSAHSGSLKK 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEVSTLGKAKTEPNKCVSQCAAFENPKGLIHGCSKDNRNDTEGFKYPLGHEVNHSRETSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; PAGES: 66-71
; DATE: 1994
; RELEVANT RESIDUES I
; RELEVANT RESIDUES I
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Best Local Similarity
Matches 221; Conserv
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APPLICANT: STEINER, MITCHELL S.
APPLICANT: ROBINSON-BENION, CHERYL L.
APPLICANT: THOMPSON, MARRILYN E.
TITLE OF INVENTION: THERAPBUTIC METHOI
TITLE OF INVENTION: PROSTATE CANCER
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (919) 419-0383 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: UNKNOWN PUBLICATION INFORMATION: AUTHORS: Mikl, Y., et. al.
TITLE: A strong candidate gene for the breast TITLE: ovarian cancer susceptibility gene
TITLE: BRCA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 39,395
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1010 100 100
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APPLICATION NUMBER: 08/61
FILING DATE: 20 FEB 1996
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JI
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ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1401, UNIVERSITY TOWER,
STREET: BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                            157
204
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SOFTWARE: WORD PERFECT 6.1 and ASCII
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                                                                                                                                                                                                                                                                                                          48 VDEPAQHQCEHFSIRGYVALL--QKKDPKFCSLSRIFHDQKKCDEHKASSSPFS--VAKF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                          VSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAE-ANTDSPMKDLQGPAQNYD 215
                                                                                                                                                                                                                      RRWDCSKCLD-----
                                                                                                                                                                                                                                                                IKEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLCKNDITKRSLQE----STRFSQLVEEL 86
                                                                                      LQETSLSVQLSNLGTV-RTLRTKQRIQPQKTSVYIELGSDSSEDTVNKATY--CSVGDQE
                                                                                                                -----KLKTSDNGTAPRTLPAKQNGT------
                                                                                                                                                                          LKIICAFQLDTGLEYANSYNFAKKENNSPEHLKDEVSIIQSMGYRNRAKRLLQSEPENPS 146
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VENTION: THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                       Conservative 174; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science
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PQGTRDEISLDSAKKAACEFSETDVTNTEHHQPSNN--
                                                                                                                                                                                                                                                                                                                                                       Score 180; DB 4; 1
Pred. No. 5.2e-05;
74; Mismatches 387;
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amino acids 1214-1223
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 1863;
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RESULT 7
US-08-986-106-2
US-08-986-106-2
; Sequence 2, Application US/08986106
; Patent No. 6177410
; Patent No. 6177410

GENERAL INFORMATION:
APPLICANT: HOLT, APPLICANT: JENSEN

HOLT, JEFFREY T. JENSEN, ROY A.

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RESULT 8
US-09-007-678B-49
Sequence 49, Application US/09007678B
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                                                                                                                                                                                                                                                                                EEHSMSPEREMG----NENIPST---
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                                                                                                                                                IANWSENCGTQSGYKLGVSTGITSHQMNRKEHFE 979
                                                                                                                                                                                                                                  HN-QYKGSTSTSYGSNLNGKIPLTFE----DLSRHQLHDLHRPLRPHPRVGVLGSLLQKE 945
                                                                                                         YKQSLPGSNCKHPEIKKQEYE 1114
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                                                                                                                                                                                             --LG-VLQPE 1092
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GENERAL INFORMATION
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; TYPE: PRT
ORGANISM: Homo sapiens
; PERTURE:
; NAME/KEY: misc_feature
; LOCATION: (1472)
; OTHER INFORMATION: Xaa=any amino acid
US-09-007-678B-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 221; Conserv
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APPLICANT: JENSEN, ROY A.
APPLICANT: PAGE, DAVID L.
APPLICANT: OBERMILLER, PA
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AVQKTPEMINQGTNQTEQNGQVMNITNSGHENKTKGDSIQNEKNPNPIESLEKESAFKTK
                                                   TKRKYSDVVDDGSS-----GSVHHTV 468
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                                                                                                                YRKKASLPNLSHVTENLIIGAFVSEPQIIQERPLTNKLKRKRRPTSGLHPEDFIKKA-DL
                                                                                                                                                                                                                                 AKVADVLDVLNEVDEYSGSSEKIDLLAS--DPHEALICKSDRVHSKSVESDIEDKIFGKT
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OBERMILLER, PATRICE S.
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Applicat Patent No. 5622829 GENERAL INFORMATION:
                                                                                                                                                                                                     APPLICANT: LYNCH, Eric
APPLICANT: SZABO, CSilla
APPLICANT: LEE, Ming
APPLICANT: LEE, Ming
TITLE OF INVENTION: GENETIC MARKERS FO
TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1093 V-----YKQSLPGSNCKHPEIKKQEYE 1114
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SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                         STREET: 4 Embarcadero Center,
CITY: San Francisco
                                                                                                                     COUNTRY: USA
                                                                                                                                          STATE: California
                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSDY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAKKLTWE------QFKATTRNSPAAT------CGAQFRPGIQAVDLTSTHVMGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IANWSENCGTOSGYKLGVSTGITSHOMNRKEHFE 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HN-QYKGSTSTSYGSNLNGKIPLTFE----DLSRHQLHDLHRELRPHPRVGVLGSLLQKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMEE-----SELDAQYLQNTFKVSKRQSFAPFSNPGNAEEECATFSAHSGSLKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEHSMSPEREMG-----NENIPST------VSTISRNNIRENVFKEASS
                                                                                                         94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08425061
                                                                                                                                                                                                                                                                                                                                    ROWELL,
                                                                                                                                                                                                                                                                                                                                                      OSTERMEYER, Beth
                                                                                                                                                                                                                                                                                                                                                                       KING, Mary-Claire FRIEDMAN, Lori
                                                                                                                                                                                            FLEHR, HOHBACH, TEST, ALBRITTON &
                                                                                                                                                                                                                                                                                                                                    Sarah
                                                                                                                                                                             Suite
                  Version #1.30
                                                                                                                                                                                                                                                                  FOR
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                                                                                                                                                                                                                                                                  AND OVARIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         894
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NAME: OSMAN, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8770
TELEFAX: (415) 494-8771
TELEX: 910 27729
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1202 amino acids
TYPE: amino acid
STEPANDEPNINGS: 41016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
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                                                                                                                                                    519
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632 SPPNCTELQIDSCSS---
                                                                                                                                                                                      430 KSSKNKTKRKYSDVVDDGSS------LMNWLN----GKKKRTGSVHHTVAHPAGNLSNK
                                                                                                                                                                                                                                                                                                      407 AKVADVLDVLNEVDEYSGSSEKIDLLASDPHEALIC----KSERVHSKSVESN-IEDKIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 NVEK----AEFCNKSKQP----GLARSQHNRWAGSKETCN---DRRTPSTEKKVDLNADP 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 VAANVSEDNTSVDVGALPEVPQ-----ITWHIEVNGADQPPSTPKLSEVVLKRNEDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 LLQIT--
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 IKEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLCKNDITKRSLQE----STRFSQLVEEL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 VDEPAQHQCEHFSIRGYVALL--QKKDPKFCSLSRIFHDQKKCDEHKASSSPFS--VAKF 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVHRENAADPCEDDRSTIPVPM------EVSMDIPVSNH------TVG---EDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKTEETLVAEQCNLTKDPNPMSGKERDQ-----VAEQCNLTKDPKPVSGQK-----CEQ
                                                                                                                                                                                                                            GKTYRKKASLP---NLSHVTENLIIGAFVTEPQIIQERPLTNKLKRKRRPTSGLHPEDFI
                                                                                                                                                                                                                                                                                                                                                                                                                    ICNE-----PCEE-----VVLKRSSKSKR----KTDKKLMKKQQHSKKRTAQ 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAE-ANTDSPMKDLQGPAQNYD 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQETSLSVQLSNLGTV-RTLRTKQRIQPQKTSVYIELGSDSSEDTVNKATY--CSVGDQE
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                                ----SEISTORCSSKGKTAGLSKGKTHSAASTKYGGESTRNGQNIHVLSAED-----Q
                                                                          SAFKTKAEPISSSISNME
                                                                                                                                                  KKA-DLAVQKTPEMINQGTNQTEQNGQVMNITNSGHENKTKGDSIQNEKNPNPIESLEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----DLNTTEKRAAERHPEKYQGSSVSNLHVEPCGTNTHASSLQHENSSLLLTKDRM 297
                                                                                                            ----KVTPTASTQHDDENDTENGLDTNMHKTDV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PQGTRDEISLDSAKKAACEFSETDVTNTEHHQPSNN--
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--SEEIKKKKYNOMPVRHSRNLQLMEGKEPATGAKK
                                                                          LELNIHNSKAPKKNRLRRKSSTRHIHALELVVSRNL
                                                                                                                                                                                                                                                                                                                                          -----AKLCRRKPKKVRLLSEIINANQVEDSRS 388
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RESULT 10
US-08-825-886-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LEE, Ming
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1086 -LG-VLQPEV-----YKQSLPGSNCKHPEIKKQEYE 1114
                                  ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         937 VLGSLLQKEIANWSENCGTQSGYKLGVSTGITSHQMNRKEHFE 979
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           NAME: OSMAN,
                                                              FILING DATE:
                                                                                                                          CLASSIFICATION:
                                                                                                                                                 FILING DATE:
                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQLHNSQYAHN-QYKGSTSTSYGSNLNGKIPLTFE----DLSRHQLHDLHRPLRPHPRVG 936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNHSRETSIEMEE------SELDAQYLQNTFKVSKRQSFAPFSNPGNAEEECATF 885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKCSIKGGSRFCLSSQFRGNETGLITPNKHGLLQNPYRI?PLFPIKSFVKTKCKKNLLEE 100:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKVSNNAED--PKDLM-----LSGERVLQTE-----RS/JESSS------ISLVPGTD 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSD 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENVFKEASSSNINEVGSSTNEVGSSIN-EIGSSDENIQAELGRNRGPKLNAMLR---
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                                                                                                                                                                                                                                                                                                                                                                                           SSEE: FLEHR, HOHBACH, TEST, ALBRITTON & T: 4 Embarcadero Center, Suite 3400 San Francisco
                                                                                                                                                                                                                                                                                                                                                                      California
                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYNCH, Eric
SZABO, Csilla
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Richard A
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                                                                                                                                                                    US/08/825,886
                                                                                08/425,061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.2%; Score 179; DB 2; Best Local Similarity 17.9%; Pred. No. 3.1e-05; Matches 222; Conservative 170; Mismatches 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 494-877
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: A --
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8770
TELEPAN: (415) 494-8771
                                        681
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TYPE: amino acid
STRANDEDNESS: si
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TREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSD
                                    SNKPNEQTSKRHDSDTFP--
                                                                                                               SPPNCTELQIDSCSS--
                                                                                                                                                                                                                                                                                               KSSKNKTKRKYSDVVDDGSS-----LMNWLN----GKKKRTGSVHHTVAHPAGNLSNK 478
                                                                                                                                                                                                                                                                                                                                     GKTYRKKASLP---NLSHVTENLIIGAFVTEPQIIQERPLTNKLKRKRRPTSGLHPEDFI
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                                                                         CQMETENSVLSHSAKVSPAEHDIQI-----
                                                                                                                                                                                       SAFKTKAEPISSSISNME-----LELNIHNSKAPKKNRLRRKSSTRHIHALELVVSRNL
                                                                                                                                                                                                                       ----KVTPTASTQHDDENDTENGLDTNMHKTDV------CQHV-----
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APPLICANT: KING,
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
APPLICANT:
                                                 ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59563-3/DJB/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8770
TELEFAX: (415) 494-8771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: GENETIC TITLE OF INVENTION: CANCER NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                           STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                        94111-4187
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SZABO, Csilla
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FRIEDMAN, Lori
OSTERMEYER, Beth
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                                                                                                                                                                                                                                                            Version #1.30
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; LENGTH: 1363 amino aci
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-061-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 VDEPAQHQCEHFSIRGYVALL--QKKDPKFCSLSRIFHDQKKCDEHKASSSPFS--VAKF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAANVSEDNTSVDVGALPEVPQ------ITWHIEVNGADQPPSTPKLSEVVLKRNEDEN 268
                                      YGTQESISLLEVSTLGKAKTEPNKCVSQCAAFENPKGLIHGCSKDNENDTEGFKYPLGHE
                                                                                                                 VKVSNNAED--PKDLM-----LSGERVLQTE-----RSVESSS-----ISLVPGTD
                                                                                                                                                                                                                                                                          SPPNCTELQIDSCSS------SEEIKKKKYNQMPVRHSRNLQLMEGKEPATGAKK
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STQEQQTHLRMEEMVTIAASSPLFSHHDDQYIAE---
                                                                                                                                                   TREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSD
                                                                                                                                                                                              SNKPNEQTSKRHDSDTFP---ELKLTNAPGSFTKCSNTSELKEFVNPSLPREEKEEKLET
                                                                                                                                                                                                                                  CQMETENSVLSHSAKVSPAEHDIQI-----MSDLHE---QSLPKKKKKQKLEV
                                                                                                                                                                                                                                                                                                                                                                          ICNE-----PCEE------VVLKRSSKSKR----KTDKKLMKKQQHSKKRTAQ 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKTEETLVAEQCNLTKDPNPMSGKERDQ-----VAEQCNLTKDPKPVSGQK-----CEQ 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----DLNTTEKRAAERHPEKYQGSSVSNLHVEPCGTNTHASSLQHENSSLLLTKDRM 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAE-ANTDSPMKDLQGPAQNYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                KKA-DLAVQKTPEMINQGTNQTEQNGQVMNITNSGHENKTKGDSIQNEKNPNPIESLEKE
                                                                          -ASSVFDTNSQQKSLASQSTQKELQGHL-----ALTTQESPHPQNFQ
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US-08-825-886-23

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RESULT 12
US-08-825-886-23
US-08-825-886-23
; Sequence 23, Applica
; Sequence 23, Seguinos
; Seguinos 5821328
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                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: KING, M:
APPLICANT: FRIEDMAN
APPLICANT: OSTERMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/825,886
                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1363 amino aci
TYPE: amino acid
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APPLICANT: LEE, Ming

APPLICANT: LEE, MI
                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                             TOPOLOGY:
                                                                                         TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQLHNSQYAHN-QYKGSTSTSYGSNLNGKIPLTFE----DLSRHQLHDLHRPLRPHPRVG: | | | : | : | : | : | : | : | : |
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LYNCH, Eric
SZABO, Csilla
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FRIEDMAN, Lori
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                                                         linear
protein
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19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.00   19.0
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US-08-425-061-24
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                                                                                                                             US-08-425-061-24
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                             Query Match
Best Local Similarity
Matches 222; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL
                                                                                                                                                                                                                                                  TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARIDA
REGISTRATION NUMBER: 36.627
REFERENCE/DOCKET NUMBER: A-59563-3/DJB/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8771
TELEPAX: (415) 494-8771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1852 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: GENETIC TITLE OF INVENTION: CANCER NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1002
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                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
 48 VDEPAQHQCEHFSIRGYVALL--QKKDPKFCSLSRIFHDQKKCDEHKASSSPFS--VAKF 103
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OSTERMEYER, Beth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEE, Ming
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SZABO, Csilla
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                                   Conservative 170;
                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/425,061
                                   Score 179; DB 1;
Pred. No. 6.2e-05;
0; Mismatches 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.30
                                                                   Length 1852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      979
                                   Indels 470;
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                                                      942 AKCSIKGGSRFCLSSOFRGNETGLITPNKHGLLQNPYRIPPLFPIKSFVKTKCKKNLLEE
                                                                                                                           886 SAHSGSLKKQSPKVTFECEQKEENQGKNESNIKPVQTVNITAGFPVVGQKDKP----VDN
                                                                                                                                                                                                                                                                     777
                                                                                                                                                                                                                                                                                                         666 Y-----ASSVFDTNSQQKSLASQSTQKELQGHL-----ALTTQESPHPQNFQ
                                                                                                                                                                                                                                                                                                                                            738 VKVSNNAED--PKDLM-----LSGERVLQTE-----RSVESSS-----ISLVPGTD
                                                                                                                                                                                                                                                                                                                                                                              606 TREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSD
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                                                                                                                                                             744 TEHWG--RKDAKKLTWE-----
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                                                                                                                                                                                                  VNHSRETSIEMEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                 SNKPNEQTSKRHDSDTFP---ELKLTNAPGSFTKCSNTSELKEFVNPSLPREEKEEKLET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKA-DLAVQKTPEMINQGTNQTEQNGQVMNITNSGHENKTKGDSIQNEKNPNPIESLEKE 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSSKNKTKRKYSDVVDDGSS-----LMNWLN----GKKKRTGSVHHTVAHPAGNLSNK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVHRENAADPCEDDRSTIPVPM-----EVSMDIPVSNH-----TVG---EDGL 429
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NFPSTIATMEASKLCDRRNAGQVVLYPKESMPATHLLRMMDPSTLASFPNYGTSSRNQME
                                                                                                                                                                                                                                STQEQQTHLRMEEMVTIAASSPLFSHHDDQYIAE-----AP-----AP-----
                                                                                                                                                                                                                                                                   YGTQESISLLEVSTLGKAKTEPNKCVSQCAAFENPKGLIHGCSKDNRNDTEGFKYPLGHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMETENSVLSHSAKVSPAEHDIQI------MSDLHE---QSLPKKKKKQKLEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SEISTQRCSSKGKTAGLSKGKTHSAASTKYGGESTRNGQNIHYLSAED-----Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----KVTPTASTQHDDENDTENGLDTNMHKTDV------CQHV-----
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                                                                                     TSTHVMGSSSNYASRQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AKLCRRKPKKVRLLSEIINANQVEDSRS
                                                                                                                                                              -QFKATTRNSPAAT-----CGAQFRPGIQAVDL
                                                                                                                                                                                                  -SELDAQYLQNTFKVSKRQSFAPFSNPGNAEEECATF
                                                                            -PVIAPLDRYAE-RAVNQVHAR
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Qy 104 RRWDCSKCLD 113 : 41:	QY 48 VDEPAQHQCEHFSIRGYVALLQKKDPKFCSLSRIFHD\2KKCDEHKASSSPFSVAKF 103	Query Match 3.2%; Score 179; DB 2; Length 1852; Best Local Similarity 17.9%; Pred. No. 6.2e-05; Matches 222; Conservative 170; Mismatches 381; Indels 470; Gaps 62;	; TOPOLOCY: linear ; MOLECULE TYPE: protein US-08-825-886-24	; SEQUENCE CHARACTERISTICS; ; LENGTH: 1852 amino acids ; TYPE: amino acid ; STRANDEDNESS: single	; TELEPHONE: (415) 494-8700 ; TELEFAX: (415) 494-8771 • ; TELEX: 910 277299 ; INFORMATION FOR SEQ ID NO: 24:	RICI NUMBI KET I	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: 08/425,061 ; FILING DATE: ; ATTORNEY/AGENT INFORMATION:	325,886	### ### ##############################	; SPATE: California ; COUNTRY: USA ; ZIP: 94111-4187 ; COMPUTER READABLE FORM:	NDENCE ADDRE SEE: FLEHR, : 4 Embarca San Francis	APPLICANT: LEE, Ming TITLE OF INVENTION: CANCER TITLE OF INVENTION: CANCER NUMBER OF SEQUENCES: 24	ROWEI LYNCI SZAB	AL INFORMATION: LICANT: KING, Mary-C	RESULT 14 US-08-825-886-24 ; Sequence 24, Application US/08825886 ; Patent No. 5801328	Qy 937 VLGSLLQKEIANWSENCGTQSGYKLGVSTGITSHQMNRKEHFE 979	Qy 882 SQLHNSQYAHN-QYKGSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPLRPHPRVG 936  1033 ENVFKEASSSNINEVGSSTN-EIGSSDENIQAELGRNRGPKLNAMLR 1085	_
QY 882 SQLHNSQYAHN-QYKGSTSTSYGSNLMGKIPLTFEDLSRHQLHDLHRPLRPHPRVG 936	NEPSTIATMEASKICDRRNAGQVVLYPKESMPATHLLRWMDPSTLASFENYGTSGRNQME	Oy 786 TSTHVMGSSSNYASRQ	OY 744 TEHWGRKDAKKLIWEQFKATTRNSPAATCGAQFRPGIQAVDL 785	Qy 708 STQEQQTHLRMEEMVTIAASSPLFSHHDDQYIAEAP743 ::::::::::::::::::::::::::::::::::::	QY 666 YASSVFDTNSQQKSLASQSTQKELQGHLALTTQESPHPQNFQ 707	QY 606 TREKQTMIDDIPMDIVELLAKNOHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSD 665 :	QY 561 CQMETENSVLSHSAKVSPAEHDIQIMSDLHEQSLPKKKKKQKLEV 605	Qy 512SEISTQRCSSKGKTAGLSKGKTHSAASTKYGGESTRNGQNIHVLSAEDQ 560	Qy 479KVTPTASTQHDDENDTENGLDTNMHKTDVCQHV	Qy 430 KSSKNKTKRKYSDVVDDGSSLMNWLNGKKKRTGSVHHTVAHPAGNLSNK 478   : : :   :::   : :	QY 389 DEVHRENAADPCEDDRSTIPVPMEVSMDIPVSNHTVGEDGL 429 : : :  :   :   :   :   :	QY 356 ADVSD	QY 318 ICNEPCEEVVLKRSSKSKRKTDKKLMKKQQHSKKRTAQ 355	Db 298 NVEKAEFCNKSKQPGLARSQHNRWAGSKETCNDRRTPSTEKKVDLNADP 346	216 VAANVSEDNTSVDVGALPEVPQITWHIEVNGADQPPSTPKLSEVVLKRNEDEN	Qy 157 VSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAE-ANTDSPMKDLQGDAQNYD 215	Qy 114KLKTSDNGTAPRTLPAKQNGTSDGCSITFVRSTFVPASVGSQK 156 :  :  :	Db. 87 LKIICAFQLDTGLEYANSYNFAKKENNSPEHLKDEVSIIQSMGYRNRAKRLLQSEPENPS 146

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US-08-480-784-2
; MOLECULE TYPE: US-08-480-784-2
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APPLICANT: Skolnic
APPLICANT: Goldgar
APPLICANT: Miki, Y
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                                                                                                                                                              APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION NUMBER: US 08/308,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                         TELEFAX: 202-962-8300 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LENGTH: 1863 amino acids
TYPE: amino acid
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APPLICANT:
APPLICANT:
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ZIP: 20005
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                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/480,784
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Shattuck-Eidens, Donna M.
Tavtigian, Sean V.
Wiseman, Roger W.
Wiseman, Roger W.
Futreal, P. Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Venable, Baetjer, Howard & Civiletti, LLP 1201 New York Avenue, N.W., Suite 1000
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Query Match Best Local Similarity

3.2%; 17.9%;

Score 179; DB 1; Pred. No. 6.2e-05;

Length 1863;

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Qy 786 Db 942	Qy 744 Db 886	Qy 708 Db 837	Qy 666 Db 777	Qy 606 Db 738	Qy 561 Db 681	Db 632		Оу 479	Db 519		Оу 389	Db 407			Ov 318		Db 245	Qу 216	Db 204	Qy 157	Db 147	Qy 114	Db 87	Qy 104	Db 31	Оу 48	Matches
TSTHVMGSSSNYASRQPVIAPLDRYAE-RAVNQVHAR	TEHWGRKDAKKLTWEQFKATTRNSPAATCGAQFRPGIQAVDL	STOROOTHLRMEEMVTIAASSPLESHHDDOYIAEAP	YALTTOESPHPONFQ   ::	TREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSD::       ::   :   :   :   :   :   :   :	CQMETENSVLSHSAKVSPAEHDIQIMSDLHEQSLPKKKKKKKKKKKKEEV	SPENCTELQIDSCSSSEEIKKKKYNQMPVRHSRNLQLMEGKEPATGAKK	SAFKTKAEPISSSISNMELELNIHNSKAPKKNRLRRKSSTRHIHALELVVSRNL	KYTPTASTQHDDENDTENGLDTNMHKTDVCQHV	CALANCET PENNINGT NOT RECORD TO STATE OF THE STATE OF T	GKTYRKKASLPNLSHVTENLIIGAFVTEPQIIQERPLTNKLKRKRRPTSGLHPEDFI GKTYRKKASLPNLSHVTENLIIGAFVTEPQIIQERPLTNKLKRKRRPTSGLHPEDFI	DEVHRENAADPCEDDRSTIPVPMEVSMDIPVSNHTVGEDGL		ADVSDAKLCRRKPKKVRLLSEIINANQVEDSRS	CERKEWNKQKLPCSENPRDTEDVPWITLNSSIQKVNEWFSRSDELLGSDDSHDGESESN	NVEKPREECNNSKOPGLAKSOHNKWAGSKETCNDKKIPSTERKVULNAUF TCNEPREECVVLKRSSKSKRKTDKKLMKKOOHSKKRTAO	GKTEETLVAEQCNLTKDPNPMSGKERDQVAEQCNLTKDPKPVSGQKCEQ	DUNTTEKRAAERHPEKYQGSSYSNLHVEPCGTNTHASSLQHENSSLLLTKDRM	VAANVSEDNTSVDVGALDEVPQITWHIEVNGADQPPSTPKLSEVVLKRNEDEN	LLQITPQGTRDEISLDSAKKAACEFSETDVTNTEHHQPSNN	VSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAE-ANTDSPMKDLQGPAQNYD	LQETSLSVQLSNLGTV-RTLRTKQRIQPQKTSVYIELGSDSSEDTVNKATYCSVGDQE	SLKTSDNGTAPRTLPAKONGTSDGCSITFVRSTFVPASVGSQK	. I.	RRWDCSKCLD	KEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLCKNDITKRSLQESTRFSQLVEEL 86	VDEPAQHQCEHFSIRGYVALLQKKDPKFCSLSRIFHDQKKCDEHKASSSPFSVAKF	222; Conservative 170; Mismatches 381; Indels 470; Gaps
821 1001	785 941	743 885	707 836	665 776	605 737	680	631	511	577	518 478	429	461	388	406	355	317	297	268	244	215	203	156	146	113	9	103	ξ

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Perfect score:
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd
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natural killer cell tumor-recognition protein - mouse
N;Alternate names: cyclophilin-related NK-tumor racognition protein; natural kil
C;Species: Mus musculus (house mouse)
C;Date: 17-Uul-1994 #sequence_revision 17-Jul-1994 #text_change 05-Nov-1999
C;Accession: B47328; I77662
R;Anderson, S.K.; Gallinger, S.; Roder, J.; Frey, J.; Young, H.A.; Ortaldo, J.R.
Proc. Natl. Acad. Sci. U.S.A. 90, 542-546, 1993
A;Title: A cyclophilin-related protein involved in the function of natural kille
A;Reference number: A47328; MUID:93133824
A;Accession: B47328
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1507 <AND>
A;Cross-references: GB:L04289; NID:9192866
A;Note: authors translated the codon AGT for residue 972 as Arg
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A;Gene: NK-TR
C;Superfamily: natural killer cell tumor-recognition
C;Keywords: alternative splicing; lymphocyte
F;60-230/Domain: cyclophilin homology <CYP>
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A;Cross-references: GB:S65998; NID:g425701; PIDN:AAB28500.1;
C;Genetics:
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A;Title: II-2 regulates the expres
A;Reference number: 157820; MUID:
A;Recession: I77662
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                    QQKSLASQSTQKELQGHLALTTQESPHPQNFQSTQEQQTHLRMEEMVTIAASSPLFSHHD
                                                                                                                                                                                                                                                                                                                                                                               SYHKREKPSESDGSAYSKYSDRSSGSSGSKGSKSSRSSSRSYTRSRSLPTSRSLSR
                                                                                                                                                                                                                                                                                                                                                                                                                            TQHDDENDTENGLDTNMHKTDVC-----QHVSEISTQRCSSKGKTAGLSK------
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                                                                                                                          I PMDIVELLAKNOHEROLMTETDCSDINRIOSKTTADDDCVIVAAKDGSDYASSVFDTNS
                                                                                                                                                                            SKYVRGREKSSRHRKYSESRSSLDYTSDSDQSHVQVYSAPEKEKQGKVEALNDKQ-----
                                                                                                                                                                                                                                                                               SPSSRSHSPNKYSDGSQHSRSSSYTSVSSDDGRRAMFRSNRKKSVTSHKRHRSNSEKTLH
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Pred. No. 0.00031;
9; Mismatches 459
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R:Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, DNA Res. 5, 169-176, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. X. The comple A;Reference number: 214142; MUID:98403880
A;Accession: T00385
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A;Molecule type: mRNA
A;Residues: 1-1983 < CSH>
A;Cross-references: EMBL:AB014524; NID:g3327061; PIDN:BAA31599.1; PID:g3327062
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C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision
C;Accession: T00385
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                                                                                                           VGALP-----EVPQITWHIE------VNGADQPPSTFKLSEVVLKRNEDENGKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ASSVFDTN--SQQKSLAS---QSTQKELQGHLALTTQE-----SPHPQNFQS---
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 QQLAFLENVKRS---
                                 WNALQLGSVSSSADFLSARNSIAQSWTRGKGKMVHPLDRFVRQDICITNKNP 1041
                                                                     SELPSCD--GN-----ESWAYRSGTKTGPRSAISI---
                                                                                                     RPHPRVGVLGSLLQKEIANWSENCGTQSGYKLGVSTGITSHQMNRKEHFEALNSGMFSAK
                                                                                                                                      NVHGDLLRKS-----HPPKVRERHFSESTSI---DNALSRLTLGNEFSVNNGYSRRFRSF
                                                                                                                                                                        PNYGTSSRNQMESQLHNSQYAHNQYKGSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPL
                                                                                                                                                                                                          -AQK------SRVSSPLASFLQQQRSASSL-----EWEPEPHLYR---SKSLKSI
                                                                                                                                                                                                                                                                            KD-----VTAAQNLVRESGAP----SPITFTSLREAEFSDNQRRLSPPF-PLEP
                                                                                                                                                                                                                                                                                                               KDAKKLTWEQFKATTRNSPAATCGAQFRPGIQAVDLTSTHVMGSSSNYASRQPVIAPLDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - AEDEMQKSAWDQPSLPEGNK - - NKTNLDD - - - LVKGENRSSVKHRLA
LTQGRLWKPSFLKNPG----FLKDDL----RNP
                                                                     -YRPIDYGIFGKE
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vacuolar protein VAC7 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein N2467; protein YNLO54w
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 *sequence_revision 03-May-1996 *text_change 07-May-1999
C;Accession: S62982; S58722; S68168
R;Bergez, P.; Dolynon, F.; Crouzet, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62975
A;Accession: S62982
A;Molecule type: DNA
A;Residues: 1-1165 <BER>
A;Cross-references: EMBL:Z71330; NID:g1301918; PID:e239893; PID:g1301921; MIPS:YNL054
A;Experimental source: strain S288C

RESULT S62982

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A;Map position: 14L
C;Function:
A;Description: required for normal vacuole inheritance and
C;Keywords: transmembrane protein; yeast vacuole
E;925-941/Domain: transmembrane #status predicted <TMN>
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
R;Bergez, P.; Dolygnon, F.; Crouzet, M.
Yeast 12, 297, 1996
A;Title: Corrigendum to: the sequence of a 44 458 bp fragment located on the left arm A;Reference number: S68168; MUID:97060022
A;Accession: S68168
A;Status: nucleic acid sequence not shown; translition not shown
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A;Cross-references: SGD:S0004999; MIPS:YNL054w
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A;Residues: 1-1165 <BEF>
A;Residues: 1-1165 <BEF>
A;Cross-references: EMBL:U12141; NID:g1314216; PID:g1098487
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
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Yeast 11, 967-974, 1995
A;Title: The sequence of a 44 420 bp fragment located on the left arm of chromosome A;Reference number: S58711; MUID:96021608
A;Accession: S58722
A;Status: nucleic acid sequence not shown; translation not shown
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A; Residues: 1-1001 <BEW>
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473 QQQQPPKQQQQQUHGITSKISAPLLNNNKKLLSRLKNSKHISTGAILNNTIATISTNPN 532
                                                         629 HERQLMTETDCSDINRIQSKTTA---DDDCVIVAAKDGSIXYAS-----SVFDTNSQ 676
                                                                                                                                                                                                                                                                                                                                                           482 PTASTQHDDENDTENGLDTNMH-----KTDVCQHVSEIS:TQRCSS------KGKTA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                           241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 HIGSVSST-NNNSNNALINHNPLSSH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 NYDVAANVSE-----DNTSVDVGALPEVPQITWHIEVNGADQPPSTPKLSEVVLKRNED 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 QKVSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNJAAEANTDSPM--KDLQGPAQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 TANTTSNVVQHNLPTIDNNLMDSDATSH-NQDHWHSDIN.XAGTSMST---SDIPTDLHLE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 RKLTVETETVEAPVANNLLL-----SNNSNVVAPNPST?SASTST-SPLHREIVDDSVA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                  --LSQQNKPKIIERPTMHVTNSREILLGENLLDDTKAKNAPANST-THDNGPVANDGLRI 297
                                                                                                                                                                                                                        SVSSSNADNHNNNKKKTSSNNNGNNSNSASNKTNADIKN;;NADLSASTSNNNAIND----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLKSSKNKTK---RKYSDVVDDGSSLM--NWLNGKKKRT3SVHHTVAHPAGNLSNKKV-T 481
                                                                                                             -DSHESNSEKPTKADFFAARLATAVGENEISDSEETFVYESAANSTKNLIFPDSSSQQQQ
                                                                                                                                                                    SDLHEQSLPKKKKKQ-----KLEVTREKQTMIDDIPMDIVELL-----AKNQ 628
                                                                                                                                                                                                                                                                      GLSKGKTHSAASTKYGGESTRNGQNIHVLSAEDQCQMETENSVLSHSAKVSPAEHDIQIM 586
                                                                                                                                                                                                                                                                                                                                PNHSNADDNENNNKMKKNKNINSGKNERNDDTSKICTTS!!KTAPSTAPLGSTDNTQALTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSANIHGPSSTSASKAFRKASAFSNNTAPSTSNNIGSNT:PAPL;----LPLPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LSNPSSSLRNKKSSLLVASN-----PAFASDVELSKKKPAVISNNMPTSNIALYQTA 191
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	32 SHHDDQYIABADTEHWGRKDAKKLTWEQPKATTRNSPAATCGAQFRPGIQAVDL
Qу	786 TSTHVMGSSSNYASRQPVIAPLDRYAER 813 :: ::
Qy	14 AVNQVHARNFPSTIATMEASKLCDRRNAGQVVLYPKESMPATHLLRMMDPSTLASFPNYG             :   : : : :
0	700 XLEGEHNKETRONSVARADEEYNSKNNKEEHGLNEYGDNNVLEEENNG 745
₽ .	DSSNVNRPQHTNLQHEFIPEDNESDENDIHSMFYYNHKNDLETKPLISDYGEDEDVDDYD
Qy	NQYKGSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPLRPHPR
рь	807 RPNATFNSYYGSASNTHELPLHGRMPSRSNNDYYDFMVGNNTGNNNQLNE-YTPLRMKRG 86
Dy Oy	5 VGVLGSILQKEIANWSENCGTQSGYKLGVSTGITSHQM-NRKEHFEALNSGMFSA
DЬ	866 QRHL-SRTNNSIMNGSIHMNGNDDVTHSNINNNDIVGYSPHNFYSRKSPFVKVK 918
Оу	989 KWNALQLGSVSSSADFLSARNSIAQSWTRGKGKMVHPLDRFVRQDIC 103
Qy	1036 ITNKNPADET 1045
RESU T345 hypo C;Sp C;Da	RESULT 5 T34513 Typothetical protein ZK783.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-19 C;Datesion: T34513
R; Fa subm A; De A; Re	R;Favello, A.; Vaudin, M. R;Favello, A.; Vaudin, M. A;Description: The EMBL Data Library, August 1994 A;Description: The segmence of C. elegans cosmid 7,8783
A; St A; Mo A; Re A; Cr	mber: Z21536
C;Ge A;Ge A;Ma A;In 350	Z21536  y; translated from GB/EMBL/DDBJ  y; translated from GB/EMBL/DDBJ  FAV> EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:Z e: strain Bristol N2; clone ZK783
Qu Be Ma	number: Z21536 : T34513 : T34513 reliminary; translated from GB/EMBL/DDBJ type: DNA 1-3507 <fav> 1-3507 <fav> sences: EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK tal source: strain Bristol N2; clone ZK783 tal source: strain Bristol N2; clone ZK783 tal 48/2; 84/1; 196/3; 303/1; 381/1; 586/1; 605/1; 1175/3;</fav></fav>
Qу	Z21536  y; translated from GB/EMBL/DDBJ  FAV- EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP: EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN000021; CESP: EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN0000021; CESP: EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN000001; GSPDB:GN000001; GSPDB:GN000000000000000000000000000000000000
OV	Z21536  y; translated from GB/EMBL/DDBJ  y; translated from GB/EMBL/DDBJ  FAV- EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK EMBL:U13646; PIDN:AC24418.1; GSPDB:GN00021; CESP:ZK EMBL:U13646; PIDN:AC2418.1; GSPDB:GN00021; CESP:ZK EMBL:U13646; PIDN:AC2488; PIDN:AC24888; PIDN:AC24888; PIDN:AC24888; PIDN:AC24888; PIDN:AC24888; PIDN:AC24888; PIDN:AC24888; PIDN:AC24888; PIDN:AC24888; PIDN:AC2

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                                RLITGTPDDLIVSVTVPSHGNRRQNITASSVPSNSTSPIILPSESLTTPQPPPTTTTTAK
                                                                                              SESHREISTVSSEPSE--PEIPLSTTVSPNVVTASSIP----SEEPILSSVTSSSTPRV
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                                                                                                                            ----RNAGQVVLYPKESMPATHLLRMMDPS--TLASFPNYGTSSRNQMESQLHNSQY---
                                                                                                                                                            APAVTVSSEASSTTLEENSSTSSPTSSEASVKLSSLFPESI-TSEAVTVSSRAPAEITMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDDIPMDIVELLAKNOHEROLMTETDCSDINRIOSKTTADDDCVIVAAKDGSDYASSVFD
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LHDLHRPLRPHPRVGVLGSLLQKEIANWSENCGTQSGYKLGVST
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                                                              -AH-NQYKGSTSTSYGSNLNGKIPLTFEDLSRHQ-----
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A;Accession: Tijuju
A;Accession: Tijuju
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Cross: references: EMBL:AF041382; NID:g2773362; PID:g2773363; PIDN:AAB96783.1
A;Cross: references: EMBL:AF041382; NID:g2773362; PID:g2773363; PIDN:AAB96783.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             microtubule binding protein D-CLIP-190 - C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13
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R;Lantz, V.A.; Miller, K.G.
J. Cell Biol. 140, 897-910, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
EQELQQLQSKSAESESALKVVQV-QLEQLQQQAAA-----SGEEGSKTVAKLHDEISQ
                                 PMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSDYASSVFDTNSQ
                                                                                                                                                                     QHVSEISTQRCSSKGKTAGLSKGKTHSAAS-TKYGGESTRNGQNIHVLSAEDQCQMETEN
                                                                                                                                                                                                       ALDDMLRLQKEGT-------EEKSTLLEKTEKELVQIKEQAAKTLQDKEQLE
                                                                                                                                                                                                                          E--RVNKSDECE-----ILQTEVRMRDEQIRELNQQLDEVTTQLNVQKA-----DSS
                                                                                                                                                                                                                                                                                                EVHRENAADPCEDDRSTIPVPMEVSM-DIPVSNHTVGEDGLKSSKNKTKRKYSDVVDDGS
                                                                                                                                                                                                                                                                                                                                                                                                            QEKMTIQQKEVESRIAEQLEEEQRLRENVKYLN----EQIATLQSELVSKDEALEKFSLS
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                                                                                                   SVLSHSAKVSPAEHDIQIM-----
                                                                                                                                     KQISDLKQLAEQEK-----LVREKTENAINQIQLEKESIEQQLALKQNELEDFQKKQSES
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9; Mismatches 35
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proliferation potential-related protein - mouse C; Species: Mus musculus (house mouse) C; Date: 11-Jan-2000 #sequence_revision 11-Jan-20(0 C; Accession: T42727 R; Witte, M.M.; Scott, R.E. submitted to the EMBL Data Library, November 1998 A; Accession: T42727 A; Accession: T42727
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A;Molecule type: mRNA
A;Residues: 1-1560 <NIT>
A;Cross-references: EMBL:U83913; NID:g3858884; PID:g3858885; PIDN:AAC72432.1
A;Experimental source: strain Balb/C
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C;Function:
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                                                                                                                                                                                                                                                                                                                                                                84 DQKKCDEHKASSSPFSVAKFRRWDCSKCLDKLKTSDNGTAPRTL---PAKQNGT-----
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                            VKKDCSKDIKSEKPASKDEKAKKPEKNKLLDSKGEKRKFKTEEKSVDKDFESSSMKISKV
                                                                                CEQICNEPCE --
                                                                                                                                                 KLSEVVLKRNEDENGKTEETLVAEQCNLTKDPNPMSGKFRDQVAEQCNLTKDPKPVSGQK
                                                                                                                                                                                       SATAKKDNVLKPSKGPQEKVD----
                                                                                                                                                                                                                      AAEANTDSPMKDLQGPAQNYDVAANVSEDNTSVDVGALFEVPQITWHIEVNGADQPPSTP
                                                                                                                                                                                                                                                                                            SDGCSITFVRSTFVPASVGSQKVSPSTQSSQGKNADRSILPKSVQEGNDSKCNAPSGKNG
                                                                                                                                                                                                                                                                                                                               NEEKGEESESFLNPELLGKFRKCRGSSGIDETKTD-----TLFVFPSREDATPVRDEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSTGTQTTIKDLQERLEITNAELQHKEKMASEDAQKIALLKTLVEAIQVANANISA 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENCGTQSGYK-LGVSTGITSHQMNRKEHF---EALNSGNFSAKWNALQLGSVSSSA 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPLRPHPF.VGVLGSLLQKEIA-----NWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDRRNAGQVVLYPKESMPATHLLRMMDPSTLASFPNYGISSRNQMESQLHNSQYAHNQYK 895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MVTIAASSPLFSHHDDQYIAEAPTEHWGRKDAKKLTWECFKATTRNSPAATCGAQFRPGI
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                                                                                                              -----LKKAKEEATKIDS--VKPSSSSQKD-EKVTGTFRKAHSKSAKEHQEAKPAKDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDETATGHKELTSKADAWSQEMLQK------FKELQELRQQLQDSQDSQTKLK
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-QHSKKRTAQADVSDAKLCRRKPKKVRLLSEIINANQVEDSRSDEV---HRENAA
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --KVNKEYAESRAEASDLQDKVKEITDTLFAELQAERSSSSALHT-KLSKF
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 213.5; [B]
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                             -EVVLKRSSKSKFKTDKKLMKKQ------
                                                                                                                                                                                                                                                           -KSVSDKDKREKLKPKVKSDKTKRK----SDG
                                                                                                                                                                                     -----SEPP---
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                                                                                                                                                               A; Introns: 34/3; 102/3;
                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                        A;Cross-references: EMBL:AL049607; GSPDB:GN00062; ATSP:F11C18.80 A;Experimental source: cultivar Columbia; BAC clone F11C18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ωy
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                                                                                                                                                                                  A; Map position:
                                                                                                                                                                                                     A; Gene: ATSP:F11C18.80
                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-852 <BEV>
                                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: T06310
                                                                      Query Match
Best Local S
Matches 174
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                                                                     Local Sinnes 174;
                                31 VLELTATPRO-----DAAAEAGVDEPAQHQCEHFSIRGY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---GKDSSGGKLPCILNPPDLPMEKELAVGQVEKSAVKPKPQLSHSSRLSSDLTRETDEA 1405
ILETVAKVRSCVVMLDLECDALLIEMFQHFLK--AIRDHHSGNVFSSMENIMTLVLEESE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSVSPSRSHSPSGSQTRSHSSSASSAGSQ-DSKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNQMESQLHNSQYAHNQYKGSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPLRPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVMGSSSNYASRQPVIAPLDRYAER--AVNQVHARNFPSTIATMEASKLCD--RRNAGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HDHKAPYETKRPCEE--TKPVDKISGKEREKHAAEARN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --HDDQYIAEAPTEHWGRKDAKKLTW---EQFKATTRNSPAATCGAQFRPGIQAVDLTST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSEQGHFKTLSQSSK-----ETRTSEKHESVRGSSNKDFTPGRDKKVDYDSRD---YS
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                                                                     h 3.8%;
Similarity 21.2%;
74; Conservative 9;
                                                                                                                                                                                                                                                                                                                                    Z15589
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                                                                                                                                                                 163/2; 205/3; 269/3; 282/3; 564/3; 602/3; 622/2;
                                                                        97;
                                                                   Score 209.5; DB 2;
Pred. No. 0.001;
7; Mismatches 282;
                                                                        Indels
                                                                                                         Length
                                  ----VALLQKK 71
                                                                        269;
                                                                      Gaps
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                                                                                                                                                                 639/3;
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                                                                                                                                                                 667/3
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3.8%; Score 208.5; DB 2; ilarity 18.4%; Pred. No. 0.002; Conservative 179; Mismatches 402;

Length Indels

1295;

Gaps

52;

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A:Molecule type: DNA
A:Residues: 1-1295 <MIL>
A:Residues: 1-1295 <MIL>
A:Cross-references: EMBL:Z70756; PIDN:CAA94789.1; GSPDB:GN00023; CESP:T06E4.1
A:Experimental source: clone T06E4
C:Genetics:
                                                                                                                                           hypothetical protein T06E4.1 - Ca
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_rev
C:Accession: T24587
R:Lloyd, C.
                                                                                         A; Reference number: Z19910
A; Accession: T24587
A; Status: preliminary; translated
                                                                                                                   submitted to the EMBL Data Library, A; Reference number: Z19910
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385/3; 481/3; 946/3; 1034/3;
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----MNKEMVDELN------AKLGDALE-----GME---ELKKSLEVSEAKV
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ascites sialoglycoprotein 1 - rat (fragments) C:Species: Rattus norvegicus (Norway rat) C:Date: 12-Apr-1995 #sequence_revision 12-Apr-19 C:Accession: A53577 R:Wu, K.; Fregien, N.; Carraway, K.L. J. Biol. Chem. 269, 11950-11955, 1994 A:Title: Molecular cloning and sequencing of the A:Reference number: A53577; MUID:94216302 A:Accession: A53577
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A;Molecule type: mmNA
A;Residuse: 1-1630 <WUA
A;Cross-references: GB:U06746
C;Keywords: glycoprotein
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             SAKVSPAEHDIQIMSDLHEQSLPKKKKKQKLEVTREKQTHIDDIPMDIVELLAKNQHERQ
                                                                     TQRCSSKGKTAGLSKGKTHSAASTKYGGESTRNGQNIHV1.SA--EDQCQME-TENSVLSH
                                                TQETSTQELTS--SQSQHTGSMKTTHNPQTTRNTEVTTT1.SASSSDQVQVETTSQTTLSD
                                                                                                         TSHAPSVSSSSPSPPSTEGTSVDTGLTTAVTTQDSTPAT::QGSLTSSSQTLSTVSPLSTS
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A; Variety: strain Z29
C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Jun-2000 C; Accession: T44231
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A:Title: Human herpesvirus 6B genome sequence: coding A:Reference number: 222734; MUID:99412318
A;Accession: T4423.... +ranclated from GB/EMBL/DDBJ
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A;Restidues: 1-1520 <DOM>
A;Cross-references: EMBL:AF157706; PIDN:AAD49674.1
A;Experimental source: strain Z29; variant B
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microtubule-associated protein homolog - fruit fly (Drosophila mela. N; Alternate names: hypothetical protein EG:49E4.1
C:Species: Drosophila melanogaster
C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-;
C; Accession: T13564
R:Spanos, L.; Papagiannakis, G.; Siden-Kiamos, I.; Louis, C.
submitted to the EMBL Data Library, April 1999
A; Description: Sequencing the distal X chromosome of Drosophila mel.
A; Reference number: 217689
A; Reference number: 217689
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Rocession: T13564
A; Residues: 1-5327 <SPA>
A; Cross-references: EMBL:AL031128; PIDN:CAA20006.1
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A;Cross-references: FlyBase:FBgn0025392
A;Introns: 24/2; 52/3; 104/3; 179/1; 232/1; 1669/3; 2566/1; 4798/3; 5:
A;Note: EG:49E4.1
C;Superfamily: Drosophila 576K microtubule-associated protein homolog
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                                   FKATTRNSPAATCGAQFRPGIQAVDLTSTHVMGSSSNYASRQPVIAPLDRYAERAVNQVH
                                                                                                                                                      RPASVVESVKDEHDKAESRRESIAKVESVIDEAGKSDSKS-SSQDSQKDEKSTLA-SKEA
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                                                                           SRRESVVESSKDDAEKSESRPESVIASGEPV--
                                                                                                            SPHPQNFQSTQEQQTHLRMEEMVTIAASSPLFSHHDDQYIAEAPTEHWGRKDAKKLTWEQ
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225; Conserv
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·RPGSVVESVTAE - - - DEKSEQQSRRESVAESVKADTKKDGKSQ
                                                                                                                                                                                       ---SSVFDT--NSQQKSLASQSTQKELQGHLALTTQE
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δÃ	Db	ΩУ	д 2	Dp Qy	Ωу	DР	DP QA	рb	7 H O	A; A; C;		2 2 2 2	R; I Suk	T34	В	Q	P Q	멍	Qy	Db Qy
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2 PCI	3 ATI	7	6 0	2	9	σ σ	5	31 VLE 68 III	Match Local Similarity nes 214; Conser	ne: CESP:F12F3. p position: 5 trons: 281/3; 3	refermenta	ion:	ption	13 ical is: Ct 29-00			0 0	8 PE:	8	5 0
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KRKTI	TDSKLEKAADTTKQIETETVVDD	RDQVI	IGADQP :  :KSD	NTDSI :  LIESF	LPKSV	SPPTD	-QKKCDEHKASSSPFSVAKFRRWD       :  :   :   KSKKSDEPEASTEEKSTTEKPTND	VDEP!	3.7%; 18.5%; ive 1	2/3;	U80022; rain Br	slated	Library,	י מון	:     :	ARN-S	GVLGSLLQKEIANWSENC	SPLGS	QYKG:	EASKLCDRRNAGQ 
KKLM	;	EQCN	PSTPI  :  -  -	KNGAAEANTDSPMKDL- : :    :   :: EKQSTEALIESKKKEVD	KVFT	)  -  -  -	RWDC:	QHQCI	Sc Pr 61;	600/	PIDN			- Caeno: gans _revisi	SVADS	SIAQSI	ENCGTO	SRRDS1	STSTS	AGQVV:
KRKTDKKLMKKQQHS	KSK	LTKDP	KLSEV	DESKI	LVESA	rev-r : : KQIPK	SKCLD	EHFSI : SEVDV	Score 2 Pred. N	3; 18	N:AAC25	rom GB	July legans	Caenorhabdit ns evision 29-0	:    KDEKSLLV	SADFLSARN-SIAQSWTRGKGKMV	TQSGYKLGVS	:: VAESI	S	LYPKE ::
KKRT	KSKKKVLKKKTIE	AEQCNLTKDPNPMSGKERDQVAEQCNLTKDPKPVSGQKC3QICN-	GALPEVP-QITWHIEVNGADQPPSTPKLSEVVLKRNEDENGKTEETLV	KNGAAEANTDSPMKDLQGPA-Q)YDVAANVSEDNTSVDV 	GKNADRSTLPKSV	PDGCSTTFY-RSTFYPASY/3SQKYSPSTQSSQ 	QKKCDEHKASSSPESVAKERRWDCSKCLDKLKTSDNG!?APRTLPAKQNGT       :  :  :  :  :  :   	VLELTATPRODAAAEAGVDEPAOHQCEHFSIRGYVALLQ·KKDPKFCSLSRIFHD :::	ore 204; DE ed. No. 0.01 Mismatches	66/3;	25885. clone		1998 cosm	is ct-			RPHPRVGVLGSLLQKEIANWSENCGTQSGYKLGVSTGIT:SHQMNRKEHFEALNSGMF	:::   :   SVAESIKHENTKDEESPLGSRRDSVAESIKSDITKGEKSPLPSKEVSRPE	NG	ARNFPSTIATMEASKLCDRRNAGQVVLYPKESMPATHLRMMDPSTLASFPNYGTSSR 
AQ	KKT EK	QKCEC	EDENG :   : DDDKS	QGPA-QHYDVAANVSE 	FSFKR	ASVISS DEI:38	KTSDNG!?APRTLPAKQNGT     ; :  :   KTSKKS\EKKTVKPKKEVTGKPLEAKK	LLQ ETE'/G	Ξ.; Ξ.;	19,14,	1; G F:L2	ענומם/	id in	elegans 1999 #t	1.00	1023	TGIT:3HQMN    : KDAT:3APPS	KGEKS		H!IL
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	SQKS	!	/TDKS	VVSE-	QEGNDSKCNAPSG          SETPDDKSRKKEG	STAN	PAKQN  :  PKKE	DAEK	ength 3	393/	:GN0002			_change			KEHFEA     KEHSRP	EVSR	DLSR	STLA:
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363	768	321	712	655	191	165	134	84 423	aps		F12F3			1999			2973			877
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Qy 627 NQHERQLMTETDCSDINRI               Db 1187 TA-EKQTKLEKDEKSTKES	Qy 539 TKYGGESTRN	408 889 453 949 949 1009	Db 769 PAESBAQKIAEVNKAKKOKEVDDNL Qy 364 CRRKPKKVRLLSEIINANQVED i   :::  : :: b 829 QKEKDEQLKLETEVVSKKSAAEKLE
NQHERQLMTETDCSDINRIQSKTTADD	TKYGGESTRNGQNIHVLSAEDQCQMETENSVLSHSAKVSPAEHDIQI	PVPMEVSMDIPVSNHTVGEDGLKSSKNKTKRKYSDVVDDGSSLMN ::::::::::::::::::::::::::::::::::::	PAESBAQKIAEVNKAKKOKEVDDNLKREAEVAAKKIADEKLKIEAEANIKKTAEVEÄAKK CRRKPKKVRLLSEIINANQVEDSRSDEVHRENAADPCEDDRSTI :   :::  : ::  :  :  :  :  :  :  :  :  :
	I 585   1127   1127   626   K 626   K 1186		K 828 I 407 A 888

RESULT 14
F90073
Fypothetical protein SA2447 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: F90073
R;Kuroda, M,;Ohta, T.; Uchiyama, I.; Baba; T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: F90073
A;Accession: F90073
A;Status: preliminary
A;Residues: 1-2271 <KUR>
A;Coross-references: GB:BA000018; PID:g13702612; PIDN:BAB43752.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A:Genetics: A; Gene: SA2447.

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RESULT 15
B71609
hypothetical protein PFB0680w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: B71609
R;Gardner, M.J; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, I
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith,
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743
A;Accession: B71609
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-665 <GAR>
A;Cross-references: GB:AE001410; GB:AE001362; NID:g3845245; PIDN:AAC71925.1; PID:g384
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0680w
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                                            SKTTADDDCVIVAAKDGSDYASSVFDTNSQQKSLASQSTQKELQGHLALTTQESPH---P 703
                                                                                             TNANKENYEKINKNSEITITKSN---
                                                                                                                                                                                                                                     KGKTHSAASTKYGGESTRNGQNIHVLSAEDQCQMETENSVLSHSAKVSPAE---HDIQIM 586
                                                                                                                                                                                                                                                                                                                                                                                   EKEKSKDM----EKLKNKQNDEKKK----DD----NEKKKNDKQDIH---
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Result
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                                                 981 HTKRA-REKSKAKKDK-KHKAPKRKQAFHWQPPLEFGDDBE--EEMNGKQVTQDPKEKRH
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                                                                                 SSNYASRQPVIAPLDRYAERAVNQVHARNFPSTIATMEA;;KLCDRRNAGQVVLYPKESMP
                                                                                                                                               DQYIAEAPTEHW--GRKDAKKLTWEQFKATTRNSPAATC(;AQFRPGIQAVDLTSTHVMGS
                                                                                                                                                                                 NSEQDVTKSRKSDPRRG---SEKEEGEASSDSESEVGQSHIK-----AKPP-----
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39; Conservative 169;
                                                                                                                 -AKPPTSTFLPGSDGAWKSRRPQSSASESESSCSNL(;-NIRGEPQKQKHSKDDLKGD
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                                                                                                                                                                                                                                                  -GKGREEGKPKPEWECPRSKKENSEDHSRDD;;V----SKGKNCAGSKWDSES
               -HLLRMMDPSTLASFPNYGTSSRNQME;;QLH--NSQYAHNQYKGSTST
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Pred. No. 0.00028;
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
101-OCT-1996 (Rel. 34, Last annotation update)
101-OCT-1996 (Rel. 34, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97060022; PubMed-8904343;
Bergez P., Doignon F., Crouzet M.;
Yeast 12:297-297(1996).
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STRAIN=S288C / FY1676;
MEDLINE=96021608; PubMed=8533472;
Bergez P., Doignon F., Crouzet M.;
Bergez P., Doignon F., Crouzet M.;
The sequence of a 44 420 bp fragment located chromosome XIV from Saccharomyces cerevisiae."
Yeast 11:967-974(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacclaromycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. SEQUENCE 1165 AA; 128140
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                                                                                                                                                              QKVSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAEANTDSPM--KDLQGPAQ 212
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TANTTSNVVQHNLPTIDNNLMDSDATSH-NQDHWHSDINRAGTSMST---SDIPTDLHLE 114
                                                      NYDVAANVSE-----DNTSVDVGALPEVPQITWHIEVNGADQPPSTPKLSEVVLKRNED 266
                                                                                                                RKLTVETETVEAPVANNLLL-----SNNSNVVAPNPSIPSASTST-SPLHREIVDDSVA
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                                                                                                                                                                                                                                                       Score 217; DB 1; Pred. No. 0.00055;
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                                                                                                                                                 --NFLYLAFVISSLLMTGFILGFLLATNKELQDVD----
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                  STANDARD;
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                  PRT;
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 InterPro; IPR001841; Znf_ring.
Pfam; PF00271; helicase_C; 1.
Pfam; PF00176; SNF2_N; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00184; RING; 1.
Zinc-finger.
ZN_FING
NP_BIND
SITE
11
                                                                                                                                               InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chromosomes.";

Proc. Natl. Acad. Sci. U.S.A. 96:13983-13988(1999).

-I- FUNCTION: COULD BE A GLOBAL TRANSCRIPTIONAL REGUL

GENE EXPRESSION BY AFFECTING CHROMATIN.

-I- SUBUNIT: PROBABLY BINDS EZH2. BINDS ANNEXIN V IN

PHOSPHATIDYLCHOLINE/PHOSPHATIDYLSERINE-DEPENDENT

PHOSPHATIDYLCHOLINE/PHOSPHATIDYLSERINE-DEPENDENT
                                                                                                                                                                                        EMBL; AF026032; AAC08741.1; -.
EMBL; 399643; CAA67962.1; -.
MGD; MGI:103067; Xnp.
InterPro; IPR001410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McDowell T.L., Gibbons R.J., Sutherland H., O'Rourke D.N. Bickmore W.A., Pombo A., Turley H., Gatter K., Picketts Buckle V.J., Chapman L., Rhodes D., Hygys D.R.; "Localization of a putative transcriptional regulator (/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jeanmougin F., Losson R., Chambon P.; and TIF1 beta RA possible involvement of TIF1 alpha and TIF1 beta control of transcription by nuclear receptors."; EMBO J. 15:6701-6715(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Transcriptional regulator ATRX (X-linked nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [3]
SUBCELLULAR LOCATION,
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Mammalia; Eutheria;
                                                         DNA repair; Nuclear
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Jeanmougin F., Losson R., Chambon P.;
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SUBCELLULAR LOCATION:
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IPR000330; SNF2_N.
IPR001841; Znf_rin
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Rodentia;
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Sciurognathi; Muridae;
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PHQ----VDGVQFMWDCCCESVEKTKKSPGSGCILAHCMCLGKTLQVVSFLHTVLLCDKL
                                                               PQNFQSTQEQQTHLRMEEMVTIAASS: : : | : : | : : | : |
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                         PTEHWGRKDAKKLTWE---OFKATTRNSPAATCGAQFRPG----IQAVDLTSTHVMGSSS
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                                                                                                                                                                           KKKKQKLEVTREKQTMIDDIPMDIVELLAKNQHERQLMTF:TDCSDINRIQS---KTTADD
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19.3%;
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Pred. No. 0.0015;
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    domain of Hum. Mol.
                                                                                                                                                                                                                                                                                SEQUENCE OF 2401-2492 FROM N.A., AND VARIANTS ATR-X. MEDILINE-95211835; PubMed=7697714; Gibbons R.J., Picketts D.J., Villard L., Higgs D.R.; "Mutations in a putative global transcriptional regulator cause inked mental retardation with alpha-thalassemia (ATR-X syndrome).
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94214473; PubMed=8162050; Gecz J., Pollard H., Consalez G., Villard L., Stayton Millasseau P., Khrestchatisky M., Fontes M.; "Cloning and expression of the murine homologue of a X-linked nuclear protein gene closely linked to PGK1 Hum. Mol. Genet. 3:39-44(1994).
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                                                                                                                                                                            Pearce A., Chapman J
Submitted (DEC-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Determination of the genomic structure a potential zinc finger helicase."; Genomics 43:149-155(1997).
                                             "Specific interaction between the
                                                                    Colleaux L.;
                                                                                        Cardoso C., Timsit
                                                                                                                                                                                                                     SEQUENCE OF 1375-2492 FROM N.A.
                                                                                                                                                                                                                                                                   Cell 80:837-845(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and characterization of a putative helicase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97386582; PubMed=9244431;
Villard L., Lossi A.-M., Cardoso C.,
Colleaux L., Schwartz C., Fontes M.;
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                                                                                                             MEDLINE=98167853;
                                                                                                                                      EZH2 BINDING
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Giovanazzi S., Bossolasco
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MEDLINE=95179111; PubMed=7874112;
Stayton C.L., Dabovic B., Gulisano M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "ATRX encodes a novel member of the SNF2 family of proteins: point to a common mechanism underlying the ATR-X syndrome.";
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MEDLINE=97123494; I
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Mammalia; Eutheria; Primates;
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  of the human EZH2 protein.";
ol. Genet. 7:679-684(1998).
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                                                                                        PubMed=9499421;
t S., Villard L.
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WEDLINE—99347960; PubMed=10417298;
MEDLINE—99347960; PubMed=10417298;
Lossi A.-M., Millan J.M., Villard L., Orellana C., Cardoso C.,
Prieto F., Fontes M., Martinez F.;
Prieto F., Fontes M., Martinez F.;
"Mutation of the XNP/ATR-X gene in a family with severe mental
"Mutation of the XNP/ATR-X gene in a family with severe mental
"Mutation of the XNP/ATR-X gene in a family with severe mental
                                                                                                                                                                                                                                                                                                                     Fichera M., Romano C., Castiglia L., Failla P., Ruberto (Greco D., Cardoso C., Fontes M., Ragusa A.; "New mutations in XNP/ATR-X gene: a further contribution genotype/phenotype relationship in ATR/X syndrome."; Hum. Mutat. 12:214-214(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96224392; PubMe Villard L., Gecz J., Ma Munnich A., Lyonnet S.;
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"Identification of a mutation in the XNP,
reported as Smith-Fineman-Myers syndrome.
Am. J. Med. Genet. 91:83-85(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pericentromeric heterochromatin and
chromosomes.";
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         Villard L., Bonino M.-C., Abidi F., Ragusa A., Be
Lossi A.-M., Seaver L., Bonnefont J.-P., Romano C
Lacombe D., Hanauer A., Philip N., Schwartz C.E.,
                                                                                                                                                                                                                retardation, spastic paraplegia demonstration that the mutation
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                                                                                                                     Curtis M.
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                                                                                                                                              MEDLINE-99326061;
                                                                                                                                                               VARIANT
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                                                MEDLINE-99219535; PubMed=10204841;
                                                              VARIANTS ATR-X E-175; 178-V--K-198 DEL;
                                                                                                        "Carpenter-Waziri syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        point mutation
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Genet. 17:146-148(1997).
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                                                                                                                                   F., Schwartz
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Lation in the XNP gene,
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                                                                                                                               PubMed=10398237;
z C.E., Carpenter
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J., Mattei J.-F.,
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                                                                                         syndrome results from
85:249-251(1999).
                                                                                                                                                                                     65:558-562(1999)
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N., Fryer A., Keppler F
Pierpont M.E., Slaney
                                                                                                                                                                                                                and skewed pattern is involved in the
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ະ , Fontes
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Query M Best Lo Matches

Match Local

Similarity

3.8%; So 21.3%; Pu tive 102;

Score Pred.

208.5; No. 0.

.004;

DB 1;

Length Indels

Mismatches

286;

165;

Gaps

31;

AKFRRWDCSKCLD

Conservative

62

RGYVALLQKKDPKFCSLSRIFHDQKKCDEHKASSSPFSV--

KAHLALEEDLNSEFRAMDAV-NKEKNTKEHKVIDAKFETKARKGEKPCALEKKDISKSEA 462

-KTSDNGTAPRTLPAKQNGTSDGCSITFVR 144

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"Molecular genetic study of japanese alpha-thalassemia/mental retardation Am. J. Med. Genet. 94:242-248(2000).
                  EMBL;
                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                         -!- DISEASE: DEFECTS IN ATRX ARE THE CAUSE OF CARPENTER-WIZIRI SYNDROME (CWS), AN X-LINKED RECESSIVE CONDITION CHARACTERIZED BY MODERATE MENTAL RETARDATION, SHORT STATURE, BRACHIDACTYLY WITH EXCESSIVE SKIN CREASES, AND WIDENING OF THE KNUCKLES.
-!- DISEASE: DEFECTS IN ATRX ARE THE CAUSE OF JUBERG-MARSIDI SYNDROME (JM). JM IS A RARE X-LINKED RECESSIVE DISEASE CHARACTERIZED BY SEVERE MENTAL RETARDATION, GROWTH FAILURE, SENSORINEURAL DEAFNESS, MICROCENITALISM AND EARLY DEATH.
-!- DISEASE: DEFECTS IN ATRX ARE A CAUSE OF SMITH-FINEMAN-MYERS SYNDROME (SFM). CLINICAL FEATURES INCLIDE SEVERE MENTAL RETARDATION, MICROCEPHALY, GROWTH FAILURE, FACIAL ANOMALIES AND BILATERAL CRYPTORCHIDISM. DUE TO THE CLINICAL OVERLAP MITH ATR-X SYNDROME, SOME PATIENTS ORIGINALLY DIAGNOSED AS HAVING SFM, MIGHT TO THE CLINICAL OVERLAP MITH ATR-X SYNDROME, SOME PATIENTS ORIGINALLY DIAGNOSED AS HAVING SFM, MIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATR-X syndrome.
J. Med. Genet.
                                      EMBL;
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                                                                                               or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS ATR-X S-179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Evaluation of a
                                                                                                                                                                                                                                                      STATURE AND CRYPTORCHIDISM.
SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
SIMILARITY: CONTAINS 1 PHD-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THALASSEMIA/MENTAL RETARDATION SYNDROME (ALSO KNOWN AS ATR-X SYNDROME). ATR-X IS AN X-LINKED DISORDER COMPRISING SEVERE PSYCHOMOTOR RETARDATION, FACIAL DYSMORPHISM, UROGENITAL ABNORMALITIES, AND ALCHA-THALASSEMIA. AN ESSENTIAL PHENOTYPIC TRAIT ARE HEMOGLOBIN H ERYTHROCYTE INCLUSIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: UBIQUITOUS.
DISEASE: DEFECTS IN ATRX ARE THE CAUSE OF X-LINKED ALPHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTING WITH HP1.
ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1,
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SUBUNIT: PROBABLY BINDS EZH2. BINDS ANNEXIN V IN A CALCIUM PHOSPHATIDYLCHOLINE/PHOSPHATIDYLSERINE-DEPENDENT MANNER (B)
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SUBCELLULAR LOCATION:
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U72937; AAB49970.2; -. U72938; AAB49971.2; -. U72935; AAB40698.1; -. U72904; AAB40698.1; JO
                                                                                                                                                                                                                                                                                                                                                                            NCLUSIONS.
                                                                                               an
                                                                                               email to license@isb-sib.ch).
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JOINED.
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syndrome (ATR-X).";
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WEDLINE=92234949; PubMed=1373717;

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Pfam; PF02395; IGA1; 1.
PRINTS; PR00921; IGASERPTASE.
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SIMILARITY: BELONGS TO PEPTII
 SRRTRRSVQTN----
                         NFQSTQEQQTHLRMEEMVTIAASSPLFSHHDDQYIAEAPTEHWGRKDAKKLTWEQFKATT
                                                                                                              PAPENSINTGSATTMTETAEKSDKPQ--METVTENDRQPEANTVADNSVANNSESS----
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                                                                                 DDCVIVAAKDGSDYASSVFDTNSQQKSLASQSTQKELQGHLALTTQE---
                                                                                                                                        SLPKKKKKQKLEVTREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTAD
                                                                                                                                                                      AKPQAQAKPQTEPAR--ENVSTVNTKEP-QSQT-----SATVSTEQPAKETSSNV-EQ
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                                                                                                                                                                                                                               PKQEQPAAKPQAQTKPQAEPARENVLTTKNVGEPQPQAQPQTQSTAVPTTGETAANSKPA
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01-FEB-1996
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P20810;
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MEDLINE=92235069;
Lee W.J., Ma H.,
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                                                                                          Biochem.
                                                                                               Uemori T., Shimojo T., Asada K., Asano
Maki M., Hatanaka M., Murachi T., Hanza
"Characterization of a functional doma"
                                                                                                                               MEDLINE-90165962; PubMed-2407243;
                                                                                                                                            SEQUENCE
                                                                                                                                                                       "Inhibition of an exon of the
                                                                                                                                                                                                    SEQUENCE OF 101-317 FROM N.A. MEDLINE=90037002; PubMed=2553724;
                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-283
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                     SEQUENCE OF 523-708 FROM TISSUE-Testis;
                                                                                                                                                                                                                                             by exon skipping.
                                                                                                                                                                                                                                                                                                                                                 Kato
                                                                                                                                                                                                                                                                                                                                                          Asada
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MEDLINE-91124109; PubMed-2577276;
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                  Submitted
                                                                      SEQUENCE
                                                                                                                                                                                                                                           "Molecular diversity in yy exon skipping.";
          MEDLINE=95038502; PubMed=7951045;
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                                                                                                                                                                                                                                   Biol.
                                                                                                                                                                                                                                                                                                                 I., Maki M., Hatanaka M., Murachi A. Cloning of human calpastatin: see and rabbit calpastatins."; nzym. Inhib. 3:49-56(1989).
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                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no restrained by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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J. Biol. Chem. 266:3968-3972(1991)
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Biochem. Mol. Biol. Int. 33:245-252(
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FUNCTION: SPECIFIC INHIBITION OF CALPAIN (CALCIUM-DEPENDENT FUNCTION: SPECIFIC INHIBITION OF CALPAIN (CALCIUM-DEPENDENT CYSTEINE PROTEESE). PLAYS A KEY ROLE IN POSTMORTEM TENDERIZATION OF MEAT AND HAVE BEEN HYPOTHESIZED TO BE INVOLVED IN MUSCLE PROTEIN DEGRADATION IN LIVING TISSUE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
      Metazoa;
                                                                                   (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 40, Last annotation updat
-associated protein 1B (MAP 1B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              562
708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -RTGSVHHTV-----AHPAGNLSNKKVTPTASTQH------DDE
                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>A</u>
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    Chordata;
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76484 MW;
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  Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN REI'. 8).; CACD759C9284I3EA CRC64;
                                                                                                                                                                                                         PRT;
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                                                                                                                 update)
                                                                                        1B) [Contains:
Vertebrata;
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.00:1;
es 284;
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Euteleostomi;
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                                                                                     MAP1 light chain
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REPEAT
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GENOMICS 22:273-280(1994).
-I- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.
PHOSPHORYLATED MAPIB MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES
THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAPIB BRIDGING OF SUBUNITS
THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAPIB BRIDGING OF SUBUNITS
THAT ACCOMPANY NEURITE EXTENSION. AND THIS BRIDGING OF SUBUNITS
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THAT ACCOMPANY NEURITES IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L06237; AAA18904.1;
MIM; 157129; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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MEDLINE=95104835; PubMed=7806212;
Lien L.L., Feener C., Fischbach N., Kunkel L.M.;
Cloning of human microtubule-associated protein
"Cloning of human microtubule associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE WITH MAPIA AND MAPIB PROTEINS.

DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules.

PTM: LC1 is coexpressed with MAPIB. It is a polypeptide generated from MAPIB by proteolyric processing. It is free to associate with both MAPIA and MAPIB. It interacts with the amino-terminal region
                                                                                                                                                                                                                              KNADRSTLPKSVQEGNDSKCNAPSGKNGAAEANTDS--PMKDLQGPAQNYDVAANVSEDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                        TSVDVGALPEVPQITWHIEVNGADQPPSTPKLSEVVLKRNEDENGKTEETLVAEQCNLTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: TO MAPIA.
                                                     DPNPMSGKERDQVAEQCNLTKDPKPVSG-----QKCEQICNEPCEEVVLKRSSKSKRKTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of MAPIB (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TWO TUBULIN SUBUNITS IN THE POLYMER, AND THI MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STABILIZING MICROTUBULES.
                                                                                                                                                                                       KHLDFLKQPLATQKDLTGQVPTPVVKQTKLKQRADSRESLKPAAKPLPSKSVRKESKE--
                                                                                                                                                                                                                                                                                      204;
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                                                                                                                                                                                                                                                                                                         Similarity
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1895
1912
1929
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                                                                                                                                                                                                                                                                                 Conservative 170;
           -KAEVAEK--QATDVKPKAAKEKTVKKETKVKPEDKKEEKEKPKKEVAKKED
                                                                                                 ETPEVT - - - KVNHVEKPPKVESKEKVMVKKDKPVKTETKPSVTEKEVPSKE
                                                                                                                                                                                                                                                                                                                                                                                               AA;
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                                                                                                                                                                                                                                                                                                                                                                                               MW.
                                                                                                                                                                                                                                                                                                      Score 196.5; DB Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                 LYS-RICH
KKEE AND
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                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                               448;
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ANK2_HI
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ANK2_HUMAN STANDARD; PRT; 3924 AA. 001484; 001485; 014848; 027 Created) 01-OCT-1996 (Rel. 25, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin,
                                                                                                                                     LT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEEHVCVSASKHSPTEDEESAKAEADAYIREKRESVASGDDRAEEDMDEAIEKGEAEQSE
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                                                                                                                                                                                                                    VSDKSATPVDEGVAEDTYSHMEGVASVSTAS
                                                                                                                                                                                                                                                                                                  PIKEDFGQEKKTDDVEAMSSQPALA-LDERKLGDVSPTQIDVSQFGSFKEDTKMSISEGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVEEHCASPEDKTLEVVSP------
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Interpro; IPR002110; ANK.

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Pfam; PF00791; ZU5; 1.
PRINTS; PR01415; ANKYRIN.
SMART; SM00248; ANK; 21.
SMART; SM00005; DEATH; 1.
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PIR; A39643; A39643.
PIR; B39643; B39643.
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Tse W.T., Menninger J.C., Yang-Feng T.L.
Lux S.E., Ward D.C., Forget B.G.;
"Isolation and chromosomal localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chan W., Kordeli E., Bennett V.; "440-kD ankyrinB: structure of the madomain and selective localization in
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"Isolation and characterization of cDNAs encoding
ankyrins reveal a family of alternatively spliced
J. Cell Biol. 114:241-253(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91302466; PubMed=1830053; Otto E., Kunimoto M., McLaughlin
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation: European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffied and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Attach integral membrane proteins telements. Also bind to cytoskeletal proteins. ALTERNATIVE PRODUCTS: 3 ISOFORMS: 1 (SHOWN HE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURON TISSUE SPECIFICITY: PLASMA MEMBRANE SPECIFICITY:
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PTM: PHOSPHORYLATED ATT .....
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SIMILARITY: CONTAINS 23 ANK REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                 ; X56957; CAA40278.1;
; X56958; CAA40279.2;
; Z26634; CAB42644.1;
; M37123; AAA62828.1;
                                                                                                                                                                                                                                         Q00421; 1AWC
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PROSITE; PS500297; ANK_REP_REGION; 1.
PROSITE; PS50017; DEXPH_DOWAIN; 1.
Cytoskeleton; Alternative splicing; Phosphoryiation.
REPEAT 95 125 ANK 1.
REPEAT 96 125 ANK 2.
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2 261 ANK 6.
3 327 ANK 8.
3 360 ANK 10.
4 26 ANK 11.
4 25 ANK 11.
4 52 ANK 12.
4 92 ANK 12.
4 92 ANK 13.
5 25 ANK 14.
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Sasanuma S.-I., Sasanuma M., Tsuchiya Y.,
Yamazaki M., Tashiro H., Eki T.,
"Analysis of the nucleotide sequence of ch
Saccharomyces cerevisiae.";
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SEQUENCE 12
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MEDLINE=95400292; PubMed=7670463;
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SIMILARITY: SOME, TO MAMMALIAN NEUROFILAMENT TRIPLET M PROTEIN
                                                                  CNAPSGKNGAAEANTDSPMKDLQGPAQNYDVAANVSEDNTSVDVGALPEVP-QITWHIEV
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                                                                                                                     GSVHHTVAHPAGNLSNKKVTPTA-STQHDDENDTENGLDTNMHKTDVCQHVSEISTQRCS
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30-MAY-2000
01-MAR-2002
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P56715;
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01-MAR-2002 (Rel. 41, Last annotation update)
0xygen-regulated protein 1 (Retinitis pigmentosa
0xetinitis pigmentosa 1 protein).
                                                                                                            Guillonneau X., Piriev N.I., Danciger M., Jacobson S.G., Farber D.B.;
*A nonsense mutation in a novel gene is as pigmentosa in a family linked to the RPI lum. Mol. Genet. 8:1541-1546(1999).
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Mammalia; Eutheria;
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MOI. Genet. 8:1541-1546(1999).
FUNCTION: COULD HAVE A ROLE IN THE PHOTORECEPTOR CELLS.
TISSUE SPECIFICITY: EXPRESSED IN REBRAIN, PLACENTA, LUNG, LIVER, SKELF
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primates;
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          IN RETINA. NOT E SKELETAL MUSCLE,
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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          264 NEDEN-----GKTEET----LVAEQCNLTKDPNPM---SGKE----
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See )
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                                                                                                                                                                                                                                                        Local Similarity
les 204; Conserv
                                                                                                                                       GSOKVSPSTQSSQGKNA--DRSTLPKS--VQEGNDSKCNAPSGKNGAAEANTDSPMKDLQ
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www-"http://www.sph.uth.tmc.edu/retnet/".
DATABASE: NAME=Mutations of the RP1 gene;
NOTE=Retina International's Scientific Newsletter;
WWW-"http://www.retina-international.com/sci-news/rplmut.htm"
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DISEASE: DEFECTS IN RP1 CAUSE RETINITIS PIGMENTOSA FORM 1 (RD1); IDISEASE: CHARACTERIZED BY CONSTRICTION OF THE VISUAL FIELDS, NIGHT BLINDNESS, AND FUNDUS CHANGES. THE DISEASE SEEMS TO BE ASSOCIATED HITT TRUNCATED (STOP OR FRAMESHIFT MUTATIONS) FORMS OF THE
                                                             -----DIEKSIIFNQDGT
                                                                                     GPAQNYDVAANV--SEDNTSVDVGALPEVPQITWHIEVNGADQPPSTPKLSEVVLK---R
                                                                                                                                                                                    AGREPF---KPGNYDIQKYL--LPARLPGISQRVYP-KGNAKSESRKI---
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SIMILARITY: CONTAINS 2
DATABASE: NAME=RetNet;
                                                                                                                      RSQIYSVSSEKTHNNDCYLDYSFVPEKYLALEKNDSQ-NLPI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00537; DCX; 2.
E; PS50309; DC; 2
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6; Mismatches
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55AEDBEC43D(A507
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SEQUENCE OF 1-142 FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-Testis;
MEDLINE-98257242; PubMed-8666295;
                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                 NCBI_TaxID=10116;
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MAPB_RAT

P15205; Q62958; Q9ER21; Q9QW92;

01-APR-1990 (Rel. 14, Created)

f 16-OCT-2001 (Rel. 40, Last sequence update)

T 16-CCT-2001 (Rel. 40, Last annotation update)

E Microtubule-associated protein 1B (MAP 1B) (NE light chain LC1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLHNSQYAHNQYKGSTSTSYGSNL--NGKIPLTFEDLSRHQLHDLHRPLRPHPRYGYLGS 940
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Craniata; Vertebrata; Sciurognathi; Muridae;

Euteleostomi; ; Murinae; Rat

Rattus

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EMBL; U52950; AAB17068.1; -.
EMBL; X60370; CAC16162.1; -.
EMBL; X60370; CAC16162.1; ALT_SEO.
PIR; S06017; S06017.
InterPro; IPR000102; MAP1B_neuraxin.
Pfam; PF00414; MAP1B_neuraxin; 10.
PROSITE; PS00230; MAP1B_NEURAXIN; 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Isolation and sequencing associated protein (MAPIB) Gene 172:307-308(1996).
                                                                                                                                                                                                                                                                          modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Spinal cord;
MEDLINE-90059871; PubMed-2555150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zauner W., Kratz J., Staunton J., Feick P., "Identification of two distinct microtubule recombinant rat MAP 1B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SPRAGUE-DAWLEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE, AND PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92347374; PubMed=1639092;
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                                                                                                                                                                                                                          tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   PTM: Phosphorylated.
SIMILARITY: TO MAPIA.
CAUTION: A C-terminal fragment of this protein (residues 1597
CAUTION: A C-terminally described as neuraxin in ref.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nerve levels are high early in development but decrease during postnatal development and are low in adults. In dorsal root ganglia levels remain high throughout development.

INDUCTION: By nerve growth factor.

DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules.

PTM: LC1 is coexpressed with MAPIB. It is a polypeptide generated from MAPIB by proteolytic processing. It is free to associate with both MAPIA and MAPIB. It interacts with the amino-terminal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: 3 different light chains, LC1, LC2 and LC3, with MAP1A and MAP1B proteins.
TISSUE SPECIFICITY: Nervous system (spinal cord, braicerebellum and cerebrum). Not expressed in liver, spl
                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of MAP1B (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE: In cerebral cortex, spinal
                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collable the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heart or muscle.
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, Schmitt B., Betz H.
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SEPTPMDEMSTPRDVMTDETNNEETESPSQEFVNITKYESSLYS---QEYSKPVVASFNG
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                 -----TQEQQTHLRMEEMVTIAA-SSPLFSHHDDQYIAEAPTEHWG
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1885
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786
                                                        -ASSVEDT----NSQQKSLASQSTQKELQ-----GHLALTTQES
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Pred. No. 0.072
66; Mismatches
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LYS-RICH.
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T -> S (I
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MAP1B 5.
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MAP1B 7.
MAP1B 8.
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GLU-RICH.
LYS-RICH
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MAP1B
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RP SEQUENCE FROM N.A.

RC STRAIN-S288C / AB972;

RA JOHNSton M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,

RA JOHNSton M., Andrews S., Brinkman R., Cooper J., Kirsten J.,

RA Favello A., Fulton L., Gastung S., Greco T., Kirsten J.,

RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,

RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,

RA JOHNSON D., Johnston L., Langston Y., Latreille P., Le T.,

RA Mardis E., Menezes S., Miller N., Nhan M., Fauley A., Peluso D.,

RA Mardis E., Menezes S., Miller N., Whan M., Fauley A., Peluso D.,

RA Rifken L., Riles L., Taich A., Trevaskis E., Vignati D.,

RA Mardis E., Wohldman P., Vaudin M., Wilson R., Waterston R.;

RA Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;

CC C., Wohldman P., Vaudin M., Wilson R., Waterston R.;

CC C. -I- FUNCTION: REQUIRED FOR MEIOTIC CHROMOSOME SYNAPSIS AND CELL CYCLE

CC CHROMOSOMES IN CLOSE APPOSITION. ZIPFER TO BRING HOMOLOGOUS

CC CHROMOSOMES IN CLOSE APPOSITION. ZIPFER TO BRING HOMOLOGOUS

FILAMENTS OF THE SYNAPTONEMAL COMPLEX.
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ZIP1_YEAST
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P31111;
01-JUL-1993 (Rel. 26, Created)
01-OCT-1996 (Rel. 34, Last sequence
15-JUL-1998 (Rel. 36, Last annotatic
Synaptonemal complex protein ZIP1.
ZIP1 OR YDR285W OR D9819.9.
                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                  or send an email to license@isb-sib.ch)
EMBL; L06487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BR1824-3B;
MEDLINE-93161412; PubMed-7916652;
Sym M., Engebrecht J.A., Roeder G.S.;
"ZIP1 is a synaptonemal complex protein chromosome synapsis.";
Cell 72:365-378(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Best Local Similarity
Matches 161; Conser
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PIR; A45173; A45173.
PIR; S30868; S30868.
SGD; S0002693; ZIP1.
Nuclear protein; Meiosis; C
DOMAIN 177 333
DOMAIN 397 438
DOMAIN 456 752
CONFLICT 55 55
      783
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                        RMMDPSTLASFPNYGTSSRNQMESQLHNSQYAHNQYKGSTSTSYGSNLNGKIPL 912
                                                      SQKRELEQKIKELEEIKNHKRNEPSKKGTQNFTKPSDSPKKNATTSNLFPNNS-AAIH--
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                                                                                                                                          HWGRKDAKKLTWEQFKATTRNSPAATCGAQFRPGIQAVDLTSTHVMGSSSNYASRQPVIA 805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKVRLQSYASNSDKINEKV------GKYKSCLETLQERIATLTSHKNNQETKLKDL--
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SPMKKCPKVDHISKSRINSSKETSKF-NDEFDLSSSSNDDLELTNPSPI
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19.3%; Pro
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333 COILED COIL (POTENTIAL).
438 COILED COIL (POTENTIAL).
752 COILED COIL (POTENTIAL).
55 T -> A (IN REF. 1).
100035 MW; 674F12625CD9DDFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 183; DB 1; Length Pred. No. 0.022; 9; Mismatches 362; Indel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Best Local Similarity
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P14873;
01-APR-1990
01-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
Microtubule-associated protein 1B (MAP 1B)
[Contains: MAPI light chain LCI].
MAPIB OR MTAPIB OR MTAP5.
MUS musculue /u-----
                                                                                                                                        REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The microtubule binding domain of microtubule-associated MAP1B contains a repeated sequence motif unrelated to that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND DOMAIN.
STRAIN-SWISS WEBSTER; TISSUE-Brain;
MEDLINE-90094539; PubMed-2480963;
Noble M., Lewis S.A., Cowan N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
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                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOTH MAP1
OF MAP1B.
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S07549; QRMSP1.
MGI:1306778; Mtap1b.
                                                                                                                                                                                                                                                                                                                                                  Pro; IPR000102; MAP1B_neuraxin. PF00414; MAP1B_neuraxin; 10.
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4 MAP1 LIG
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                                                                                   MAP1B 10.
LYS-RICH
KKEE AND
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Pred.
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MAP1B 3.
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AND KKEI/V REPE
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                               LGSVSSSADFLSARNSTAQSWTRGK
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VVSPSQSVTGSAGHTPYYQSPTDEK
                                                                                                                                                                                         TNNEETESPSQEFVNITKYESSLYSQEYSKPAVASFNGLSEGSKTDATDGKDYNASASTI
                                                                                                                                                                                                                                                      GG-SESEATASDEENREDQ----PEEFTATSGYTQSTIEISSEPTPMDEMSTPRDVMSDE
                                                                                                                                                                                                                                                                                                                     EEQYGYLGTSAKQPGIQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTNSQQKSLASQSTQKELQGH---LALTTQESPHPQNFQSTQEQQTHLRMEEMVTIAASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLMS-----SPEDLTKDFEELKAEEIDVAKDIKPQ-LELIEDEEKLKETQPGEAYVIQKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVLSHSAKVSPAE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGKLKDKGKVKVIKKEGKTTEAAATAVGTAAT----TAAVVAAAGIAASGPVKELEAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEPKKEIKKISKDI-----KKSTPQSDTK-----KPSALKPKVAKKEESTKKEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGKKKRTGSVHHTVAHPAGNLSNKKVTPTASTQHDDENDTENGLDTNMHKTDVCQHVSEI
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                                                              KTPLGERSVNFSLTPNEIKVSAEGEARSVSPGVT - - QAVVEEH
                                                                                           GSLLQKEIANWS----ENCGTQSGYKLGVSTGITSHQMNRKEHFEALNSGMFSAKWNALQ
                                                                                                                            SPPSSMEEDKFSKSALRDAYCSEEKELKASAELDIKDVSDERLSPAKSPSLSPSPPSPIE 126:
                                                                                                                                                                                                                        FPNYGTSSRNQ-----MESQLHNSQYAH-----
                                                                                                                                                                                                                                                                                                                                                                                                                  PLFSHHDD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STQRCSSKGKTAGLSK-GKTHSAASTKYGGESTRNGQNIHVLSAEDQC-----QMETEN
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                                                                                                                                                                                                                                                                                      STIATMEASKLCDRRNAGQVVLYPKE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----HDIQIMSDLHEQSLPKKKKKQKLEVTREKQTMIDDIP
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                                                                                                                                                         SYGSNLNGKIPLTFEDLSRHQLHDLHRP-LRPHPRVGVL
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                               1019
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                                                                                                                                                                                                                                                                                       SMPATHLLRMMDPSTLAS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -EVAEKQATESKPKVTKD
                                                                                                                                                                                                                                                                                                                       -----ASSIHDETLP
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P531_HUMAN ID P531_HUMAN AC Q12888; DT 15-JUL-1998 DT 16-OCT-2001

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Matches 180
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MIM; 605230; ...

InterPro; IPR001357; BRCT.

Pfam; PP00533; BRCT; 2.

SMART; SM00292; BRCT; 2.

PROSITE; PS50172; BRCT; 2.

Nuclear protein; Transcription regulation; A: Nuclear Protein; Transcription RT 1.

Nuclear Protein; Transcription RT 1.

Nuclear Protein; Transcription RT 1.

Nuclear Protein; Transcription RT 1.

Nuclear Protein; Transcription RT 1.

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Nuclear Protein; Transcription RT 1.
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149
                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98421532; PubMed-9748285; Iwabuchi K., Li B., Massa H.F., Trask B.J., I "Stimulation of p53-mediated transcriptional p53-binding proteins, 53BP1 and 53BP2."; J., Biol. Chem. 273:26061-26068(1998).
                                               221
                                                                                                   161
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TISSUE=Skeletal mus
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Mammalia; Eutheria;
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                                                        GPAQNYDVAANVSEDNTSVDVGALPEVPQITWHIEVNGALQPPS
                                             QSNEDIPIAEQSSKD----
                                                                                         EDTASSQLGFGVLELSQSQDVEENTVPYEVDKEQLQSVTTNSGYTRLSDVDANTAIKHEE
                                                                                                         DEHKASSSPFSVAKFRRWDCSKCLDKLKTSDNGTAPRTLFAKQNGTSDGCSITFVRSTFV 148
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                                                                                                                                                                                               PVLDVVSNPEQTAGEERGDGNSGFN--EHLKENKVADPVISSNLDTCGSISQVI---EQL
                                                                                                                                                                                                                        PVLELTATPRODAAAEAGVDEPAQHQCEHFSIRGYVALL(KKDPKFC-SLSRIFHDQKKC
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Metazoa; Chordata; C
Metazoa; Primates; (
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llarity 18.6%;
Conservative 1:
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54 POLY-GLU.
213573 MW; 13E2CC8A265F9D2A CRC64;
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-binding protein 1 (p53-binding
                                      ----IPVTAQPSKDVHVVKEQNPPPARSEDMPFSPKASVAA
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Pred. No. 0.073
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Catarrhini; Hominidae
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                                    "CENP-E mitosis.
                                        SEQUENCE FROM N.A.

MEDLINE-93024922; PubMed-1406971;
Yen T.J., Li G., Schaar B.T., Szii
"CENP-E is a putative kinetochore
mitosis.";
                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
CHARACTERIZATION
                                                                                                                                                                                   01-JUL-1993
30-MAY-2000
                         Nature
                                                                                                                                                                        Centromeric
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01-JUL-1993
                                                                                                                                                  Homo
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                     359:536-539(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                         -QKLAILDQELEH-----KEQEAWEE--ATSEDSSVVIVDVKEPSPRVDVSCEPLEGV
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                                                                                                                        Primates;
                                                                                                                                  Chordata;
                                                                                                                                                                    Last sequence upo
Last annotation of CENP-E protein)
                                                                                                                                                                                                            Created)
                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                          Szilak
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Chan G.K.T., Schaar B.T., Yen T.J.;

Chan G.K.T., Schaar B.T., Yen T.J.;

Chan G.K.T., Schaar B.T., Yen T.J.;

Chan G.K.T., Schaar B.T., Yen T.J.;

Characterization of the kinetochore binding domain of CENP-E reveals interactions with the kinetochore proteins CENP-F and hBUBRI.";

J. Cell Biol. 143:49-63(1998).

J. Cell Biol. 143:49-63(1998).

FUNCTION: MINIS-END DIRECTED MICROTUBULE MOTOR. PROBABLE KINETOCHORE MOTOR. ACCUMULATES JUST BEFORE MITOSIS AT THE G2 PHASE OF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT AND/OR SPINDLE ELONGATION.

1. SUBCURIT: INTERACTS WITH CENP-F AND BUBRI KINASE.

1. SUBCURIT: INTERACTS WITH CENP-F AND BUBRI KINASE.

1. SUBCURIT: ASSOCIATES WITH KINETOCHORES DURING CONGRESSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE, AND IS QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
NP_BIND
SEQUENCE
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DOMAIN 1 335
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PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.

Motor protein; Cell division; ATP-binding; Coiled coil; Mitosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR001752; kinesin.
Pfam; PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z15005; CAA78727.1; -. PIR; S28261; S28261. HSSP; P17119; 3KAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-98437347; PubMed-9763420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 117143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microtubule motor.
          2025
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Thrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.;
"Mitotic HeLa cells contain a CENP-E-associated minus end-directed
microtubule motor.";
                                                                                                                                                                                                                                                                                                                         141
                                                                                                                                                                                                                                                                                                                                                                                                                                                        87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 VLELTATPRQDAAAEAGVDEPAQHQCEHFSIRGYV----ALLQKKDPKFCSLSRIFHDQK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                               NLEEMK-----SVMKERDNLRRVEETLKLERDQLKESLQETKARDLEIQQE------
                                                                                                                                                                                                                                                                                                                                                                                                                       KCDEHKASSSPFSVAK----FRRWDCSKCL--DKLKTSDNGTAPRTLPAKQNGTSDGCSI 140
LHESLEEIRIVAKERDELRRIKESLKMERDQFIATLREMIARDRQNHQVKPEKRLLSDGQ
                                                                                                                                                                                          DSPMKDLQGPAQNYDVAANVSEDNTSVDVGALPEVPQITWHIEVN-----GADQPPSTPK
                                                                                                                                                                                                                                                                                                                   TFVRSTFVPASVGSQKVSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAEANT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IQELKANEHQLITLKKDVNETQKKVSEMEQLKKQIKDQSLTLSKLEIENLNLAQELHE-- 1879
                                                            LSEV-----VLKRNEDENGKTEETLVAEQCNLTKDPNPMSGKERD--QVAEQCNLTKDPK 308
                                                                                                                                                                                                                                                       -----LKTARMLSKEHKETVDKLREKISEKTIQISDIQKDLD-----KSKDELQKKIQ 1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 18.9
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14:918-926(1995).
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312087 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.3%;
                                                                                                                        -LLRVKED-VNMSHKKINEMEQLKKQFEPNYLCKCEMDNFQLTKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 181.5; D
Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KINESIN-MOTOR.
COILED COIL (POTENTIAL).
GLOBULAR (POTENTIAL).
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W; CEFC13880C8C8CB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283;
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2084
                                                                                                                           2024
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В	Qy	В	Qγ	뮹	Qy	В	ΩУ	В	Qy	В	Qy	В	Qγ	В	Οy	В	Qy	В	Qy	Ъ	Qγ	В	Qγ
2626	864	2585	806	2548	746	2491	706	2444	651	2398	600	2338	559	2288	503	2239	455	2190	399	2141	343	2085	309
SSLGLCPEVQNAGAESVDSQ 2645	STLASFPNYGTSSRNQMESQ 883	PKSLPSPHPVRYFDN 2625	PLDRYAERAVNOVHARNEPSTIATMEASKLCDRRNAGQVVLYPKESMPATHLLRMMDP 863	TWKERTLKREAHKQVTCENSPKSPKVTGTASKKKQIT 2584	HWGRKDAKKLTWEQFKATTRNSPAATCGAQFRPGIQAVDLTSTHVMGSSSNYASRQPVIA 805	TCGGGSGIVQNTKALILKSEHIRLEKEISKLKQQNEQLIKQKNELLSNNQHLSN-EVK 2547	FQSTQEQQTHLRMEEMVTTAASSPLFSHHDDQYIAEAPTE 745	ISATKATVEYQKEVIRLLRENLRRSQQAQDTSVISEHTDPQPSNKPL 2490	ADDDCVIVAAKDGSDYASSVFDTNSQQKSLASQSTQKELQGHLALTTQESPHPQN 705	KETIQVLQDKVALGAKPYKEEIEDLKMKLVKIDLEKMKNAKEFEKE 2443	KQKLEVTREKQTMIDDIPMDIVEL-LAKNQHERQLMTETDCSDINRIQSKTT 650	TQLTTEKIRELENSLHEAKESAMHKESKIIKMQKELEVTNDIIAKLQAKVHESNKCLEKT 2397	DQCQMETENSVLSHSAKVSPAEHDIQINSDLHEQSLPKKKK 599	KEWEQDLKSLKEKNEKLFKNYQTLKT-SLASGAQVNPTTQDNKNPHVTSRA 2337	HKTDVCQHVSEISTQRCSSKGKTAGLSKGKTHSAASTKYGGESTRNGQNIHVLSAE 558	NTRFDIEKLKNGIQKENDRICQVNNFFNNRIIAIMNESTEFEERSATIS 2287	NGKKKRTGSVHHTVAHPAGNLSNKKVTPTASTQHDDENDTENGLDTNM 502	DLKLNQNMDLHIEEILKDFSESEFPSIKTEFQQVLSNRKEMTQFLEEWL 2238	PCEDDRSTIPVPMEVSMDIPVSNHTVGEDGLKSSKNKTKRKYSDVVDDGSSLMNWL 454	YVTKIKEEQHECINKFEMDFIDEVEKQKELLIKIQHLQQDCDVPSRELR 2189	MKKQQHSKKRTAQADVSDAKLCRRKPKKVRLLSEIINANQVEDSRSDEVHRENAAD 398	QHLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFHRIMKKLKYVLS 2140	PVSGQKCEQICNEPCEEVVLKRSSKSK

Search completed: September 16, 2002, 22:35:04 Job time: 658 sec

COLOGO MANTO TENDOSHI